



#5

## Sequence Listing

<110> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan I.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.

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                   110                  115                  120  
 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu  
                   125                  130                  135  
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro  
                   140                  145                  150  
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val  
                   155                  160                  165  
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys  
                   170                  175                  180  
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys  
                   185                  190                  195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys  
200 205 210

Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala  
215 220 225

Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu  
230 235 240

Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser  
245 250 255

Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His  
260 265 270

Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys  
275 280 285

Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala  
290 295 300

Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn  
305 310 315

Pro Lys Ala Val

<210> 11  
<211> 2720  
<212> DNA  
<213> Homo sapiens

<400> 11  
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gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggaggc 100  
gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
gccgcctcat cgggacttca tctcggtgac gctgagcttt ggagagagct 200  
atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300  
gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
gggttaaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga 450  
caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600  
ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750  
 agtgcacatg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800  
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
 gtgtccaggt ccttcagtga gtgggtttggc ctcggtctca cactgatcga 900  
 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950  
 ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000  
 aacctgtttg agagcacgat ccgcacatctg ggggggctcc tgagtgccta 1050  
 ccacctgtct ggggacagcc tcttctgag gaaagctgag gatctttgaa 1100  
 atcggctaata gcctgccttc agaacacat ccaagattcc ttactcggat 1150  
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 cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
 gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300  
 cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
 caatacccaac agtggcctct tcacccacct gggcgatttc acgctgggag 1400  
 ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450  
 gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500  
 tgtcagaacg cacctgctgc ggactccga gccagtaag ctcacctttg 1550  
 tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600  
 tgcttctgc cagggacgct ggctctgggc gtctaccacg gcctgccgcg 1650  
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 caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgag 1850  
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900  
 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950  
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
 tcctggggga gacgtcaag tatctgttct tgctcttctc cgatgacca 2050  
 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccacctctt 2100



gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150  
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 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250  
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 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
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 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450  
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctcgtgaagc 2500  
 ctcagatgtc cccaatcaa ggggtctggag gggctgccgt gactccagag 2550  
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 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
 tagctcacgg gcccctccag tggaatgggt cttttcgggtg gagataaaag 2700  
 ttgatttgct ctaaccgcaa 2720

<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

<400> 12  
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 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
 20 25 30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro  
 35 40 45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
 50 55 60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
 65 70 75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
 80 85 90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
 95 100 105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys  
 110 115 120  
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val  
 125 130 135  
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro  
 140 145 150  
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro  
 155 160 165  
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly  
 170 175 180  
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro  
 185 190 195  
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly  
 200 205 210  
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg  
 215 220 225  
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln  
 230 235 240  
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp  
 245 250 255  
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly  
 260 265 270  
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe  
 275 280 285  
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile  
 290 295 300  
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser  
 305 310 315  
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu  
 320 325 330  
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu  
 335 340 345  
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn  
 350 355 360  
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser  
 365 370 375  
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr  
 380 385 390  
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395 400 405  
 Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala  
 410 415 420  
 Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys  
 425 430 435  
 Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe  
 440 445 450  
 Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr  
 455 460 465  
 Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu  
 470 475 480  
 Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg  
 485 490 495  
 Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val  
 500 505 510  
 Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu  
 515 520 525  
 Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly  
 530 535 540  
 Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr  
 545 550 555  
 Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu  
 560 565 570  
 Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val  
 575 580 585  
 Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr  
 590 595 600  
 Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys  
 605 610 615  
 Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe  
 620 625 630  
 Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln  
 635 640 645  
 Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe  
 650 655 660  
 Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp  
 665 670 675  
 Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala  
 680 685 690

His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

B1  
<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagcctgtg tccaggtcct tcagtgaagt gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
ggcgccgcgt aggcccgga ggccgggccc gccgggctgc gagcgccctgc 50  
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150  
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgtctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
 cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400  
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450  
 gcaccacatc tacgtgctca accagggtgga ccacttcagg ttcaaccggg 500  
 cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550  
 attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
 B1 tggctttcct gaggtgggc ccttcacgt ggcctccccg gagctccacc 650  
 ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700  
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750  
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800  
 ttttcgccc ctcgggaatc acaactgggt acaagacatt tcgccacctg 850  
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900  
 acaggagcag ttcaagggtg acaggaggagg aggcctgaac actgtgaagt 950  
 accatgtggc ttcccgcaact gccctgtctg tgggcggggc cccctgcact 1000  
 gtcctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050  
 attcagctga gctggatgga cagtgaggaa gcctgtacct acaggccata 1100  
 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150  
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccaccc 1200  
 ggccgccaag gcaggcttg gctgggcccag gacacgtggg gtgcctggga 1250  
 cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300  
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350  
 cccaggcctg tgggtagtgg ggagggctga acaggacaac ctctcatcac 1400  
 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450  
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens  
 <220>

<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25, 65-71, 247-253, 285-291, 303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp
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Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser
				20					25					30
Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser
				35					40					45
Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala
				50					55					60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys
				65					70					75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp
				80					85					90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe
				95					100					105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser
				110					115					120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp
				125					130					135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu

	140		145		150
Glu Ser Ser Asn	Ser Thr Asp Tyr Ile	Ala Met His Asp Val	Asp		
	155		160		165
Leu Leu Pro Leu	Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu	Ala		
	170		175		180
Gly Pro Phe His	Val Ala Ser Pro Glu	Leu His Pro Leu Tyr	His		
	185		190		195
Tyr Lys Thr Tyr	Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln	His		
	200		205		210
Tyr Arg Leu Cys	Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp	Gly		
	215		220		225
Arg Glu Asp Asp	Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly	Leu		
	230		235		240
Gln Leu Phe Arg	Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr	Phe		
	245		250		255
Arg His Leu His	Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys	Arg		
	260		265		270
Ile Ala Ala Gln	Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu	Gly		
	275		280		285
Gly Leu Asn Thr	Val Lys Tyr His Val	Ala Ser Arg Thr Ala	Leu		
	290		295		300
Ser Val Gly Gly	Ala Pro Cys Thr Val	Leu Asn Ile Met Leu	Asp		
	305		310		315
Cys Asp Lys Thr	Ala Thr Pro Trp Cys	Thr Phe Ser			
	320		325		

<210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
 gcgaacgctt cgaggagtcc tgg 23

<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-24  
<223> Synthetic construct

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450  
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18



<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly  
1 5 10 15  
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30  
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45  
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60  
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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cagcggacaa aggagcatgt ccgcgccggg gaaggcccgt cctccggccg 100  
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150  
ggctccgggg cggcccgcta ggccagtgcg ccgcgcgtcg ccccgagggc 200  
cccggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgcagc 250  
cgccgctggt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300  
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tggtgtgcag cagcctggaa ctgcgcgagg tctgcccccc agatactctg 450  
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500  
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550  
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600  
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650  
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700  
atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750  
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800  
gtggatgcat cgctgggtaa aggagaagaa catcacggta cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900  
 caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950  
 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000  
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050  
 gatgggagaa tagttgaaac cgatgaatcg caaggatatt ttgttgaaaa 1100  
 gaacatgatt cacaactgct ccttgattgc aagtgcccta accatttcta 1150  
 atattcaggc tggatctact ggaaattggg gctgtcatgt ccagaccaa 1200  
 cgtgggaata atacgaggac tgtggatatt gtggtattag agagttctgc 1250  
 acagtactgt cctccagaga ggggtgtaaa caacaaagggt gacttcagat 1300  
 ggcccagAAC attggcaggc attactgcat atctgcagtg tacgcggaac 1350  
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400  
 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450  
 gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500  
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 tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650  
 aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700  
 tgatgaacgt gtctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750  
 ggattgtgca gtgtcttcag cgcattgcta cctaccggct agccggtgga 1800  
 gctcacgttt attcaacata ttcacccaat attgctctgg aagcttatgt 1850  
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900  
 tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950  
 gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000  
 attttcgagt ctggcactaa aggtatgtta cattctgcaa tcatttaaga 2050  
 ctatttacag ttaaattaga atgctccaaa tgttctgctt cgcaaaataa 2100  
 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150  
 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200  
 ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250  
 gaaattacat ttataactg cagtgggtata aatgcaaata tactattgtt 2300

acatgtgaaa aaatttttatt tgacttaaaa gtttatttat ttgttttttt 2350  
 gtccttgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400  
 atgagccttt ggcaactgcg ctgccaagcc tagtggagaa gtcaaccctg 2450  
 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500  
 acacaaatat gtcatatatc tttttttaaa aaaagtattt cattgaagca 2550  
 agcaaatga aagcattttt actgattttt aaaattgggtg ctttagatat 2600  
 atttgactac actgtattga agcaaataga ggaggcacia ctccagcacc 2650  
 ctaatggaac cacatttttt tcacttagct ttctgtgggc atgtgtaatt 2700  
 gtattctctg cggtttttaa tctcacagta ctttatttct gtcttgcccc 2750  
 tcaataatat cacaacaat attccagtca ttttaatggc tgcataataa 2800  
 ctgatccaac aggtgttagg tgttctggtt tagtgtgagc actcaataaa 2850  
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<400> 24  
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 1 5 10 15  
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
 20 25 30  
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
 35 40 45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
 50 55 60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
 65 70 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
 80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser  
 95 100 105  
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile  
 110 115 120  
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp  
 125 130 135  
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg  
 140 145 150  
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe  
 155 160 165  
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg  
 170 175 180  
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile  
 185 190 195  
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg  
 200 205 210  
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val  
 215 220 225  
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu  
 230 235 240  
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe  
 245 250 255  
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp  
 260 265 270  
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu  
 275 280 285  
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His  
 290 295 300  
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln  
 305 310 315  
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg  
 320 325 330  
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser  
 335 340 345  
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp  
 350 355 360  
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln  
 365 370 375  
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

	380		385		390
Gln Asp Glu Arg	Lys 395	Ala Trp Arg Arg	Cys 400	Asp Arg Gly Gly	Phe 405
Trp Ala Asp Asp	Asp 410	Tyr Ser Arg Cys	Gln 415	Tyr Ala Asn Asp	Val 420
Thr Arg Val Leu	Tyr 425	Met Phe Asn Gln	Met 430	Pro Leu Asn Leu	Thr 435
Asn Ala Val Ala	Thr 440	Ala Arg Gln Leu	Leu 445	Ala Tyr Thr Val	Glu 450
Ala Ala Asn Phe	Ser 455	Asp Lys Met Asp	Val 460	Ile Phe Val Ala	Glu 465
Met Ile Glu Lys	Phe 470	Gly Arg Phe Thr	Lys 475	Glu Glu Lys Ser	Lys 480
Glu Leu Gly Asp	Val 485	Met Val Asp Ile	Ala 490	Ser Asn Ile Met	Leu 495
Ala Asp Glu Arg	Val 500	Leu Trp Leu Ala	Gln 505	Arg Glu Ala Lys	Ala 510
Cys Ser Arg Ile	Val 515	Gln Cys Leu Gln	Arg 520	Ile Ala Thr Tyr	Arg 525
Leu Ala Gly Gly	Ala 530	His Val Tyr Ser	Thr 535	Tyr Ser Pro Asn	Ile 540
Ala Leu Glu Ala	Tyr 545	Val Ile Lys Ser	Thr 550	Gly Phe Thr Gly	Met 555
Thr Cys Thr Val	Phe 560	Gln Lys Val Ala	Ala 565	Ser Asp Arg Thr	Gly 570
Leu Ser Asp Tyr	Gly 575	Arg Arg Asp Pro	Glu 580	Gly Asn Leu Asp	Lys 585
Gln Leu Ser Phe	Lys 590	Cys Asn Val Ser	Asn 595	Thr Phe Ser Ser	Leu 600
Ala Leu Lys Val	Cys 605	Tyr Ile Leu Gln	Ser 610	Phe Lys Thr Ile	Tyr 615

Ser

<210> 25  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220> .  
 <221> Artificial Sequence  
 <222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100  
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaatcggga 150  
aaaaagaaaa cattcgtctt ttgggagAAC agattatTTT gactgagcaa 200  
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250  
atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300  
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350  
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400  
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450  
tttgaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500  
tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600  
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 gtggagggag agacgctcct gatcgtcgaa tcc 683

<210> 29  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-21  
 <223> Signal peptide.

<400> 29  
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu  
 1 5 10 15  
 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp  
 20 25 30  
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
 35 40 45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
 50 55 60  
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
 65 70 75  
 Lys Gly Ser Gln Lys Ser  
 80

<210> 30  
 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
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 tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100  
 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggttaaccg 150  
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200  
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250  
 ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgtcgg tggctagcgt 300  
 gggcgccctgg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350  
 tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400  
 caggcccgtt tccccctgtc ttggcgcaac ttccccatca ccttcgcctg 450

ctatgcggcc ctctttctgcc tctcggcctc catcatctac cccaccacct 500  
 atgtccagtt cctgtcccaac ggccgttcgc gggaccacgc catcgccgcc 550  
 accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600  
 gacccggggc cggcccggcg agatcactgg ctatatggcc accgtaccgc 650  
 ggctgctgaa ggtgctggag accttcgttg cctgcatcat cttegcgttc 700  
 atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtgcgt 750  
 ggcggtgtac gccatctgct tcatacctagc ggccatcgcc atcctgctga 800  
 acctggggga gtgcaccaac gtgtaccaca tccccctccc cagcttcctg 850  
 tcggggctgg ccttgctgtc tgtcctcctc tatgccaccg cccttgttct 900  
 ctggcccctc taccagttcg atgagaagta tggcggccag cctcggcgct 950  
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 gaccgcccac tggctgtggc catcctgacg gccatcaacc tactggcgta 1050  
 tgtggctgac ctggtgcact ctgcccacct ggtttttgtc aaggtctaag 1100  
 actctcccaa gaggtcccg tccccctccc aacctcttg ttcttcttgc 1150  
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 tgcactctaa ccagttcttg gatgcatctt ctccctccc ttccctcttg 1300  
 ctgtttcctt cctgtgttggt tttgttgccc acatcctgtt ttcacccctg 1350  
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 gattctcact ctgtggccca ggctggagtg cagtgggtgc atctcagctc 1450  
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 caagtagctg ggaggacagg tgtgagctgc cgcaccacgc ctgtttctct 1550  
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attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950  
 gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000  
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050  
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<210> 31  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
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 35 40 45  
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
 50 55 60  
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
 65 70 75  
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
 80 85 90  
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
 95 100 105  
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr  
 110 115 120  
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp  
 125 130 135  
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala  
 140 145 150  
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile  
 155 160 165  
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
 170 175 180  
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
 185 190 195  
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr  
 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu  
 215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
 230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu  
 245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln  
 260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr  
 275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr  
 290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala  
 305 310 315

His Leu Val Phe Val Lys Val  
 320

<210> 32  
 <211> 3680  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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 ttccaccatg ttggccaggc tggctcttgaa ctcgtgacct catgatccgc 100  
 tcacctcggc ctcccaaagt gctgggatta caggcatgag ccactgacgc 150  
 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200  
 taaacattgg gcactacagt gacccaaaaca gactgaattc cccaagagcc 250  
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300  
 ttattactca ctatgactaa gggtcacaaa tgggggtacgt tgatggagag 350  
 tgatttggtta agagactaca gagggaggac agactaccaa gagggggggcc 400  
 aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450  
 gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500  
 cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550  
 ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600  
 aagggaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650  
 gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700

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 caaggtgaat gttggagaca cagtcgcgat gctgccaag tcccggcgag 1300  
 ccctaactat ccaggagatc gctgcgctgg ccaggctctc cctgcatggt 1350  
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 gggcgaacaa gaggtctgct ttgcagcagg agtggctgag cagtttgcca 1800  
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B1

cgcagcctgg gccactgga ggcccaggac tcactctaca actcgcccct 2200  
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 cacccttttc ctggccccct aatggggcct gggccctttc ccaaccctc 3100  
 ctaggatgtg cgggcagtgt gctgggcctt cacagccagc cgggctgccc 3150  
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 tgtgccagtg agtgacagtc atgagggagt gtctcttctt ggggaggaaa 3350  
 gaaggtagag cctttctgtc tgaatgaaag gccaaaggcta cagtacaggg 3400  
 cccgccccca gccagggtgt taatgccac gtagtggagg cctctggcag 3450  
 atcctgcatt ccaaggtcac tggactgtac gtttttatgg ttgtgggaag 3500  
 ggtgggtggc tttagaatta agggccttgt aggctttggc aggtaagagg 3550  
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ggctcattag gtgtttatatt tggtctatatt aagaatttgt tttattaaat 3650

taatataaaa atctttgtaa atctctaaaa 3680

<210> 33  
<211> 335  
<212> PRT  
<213> Homo sapiens

<400> 33

Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro  
1 5 10 15  
Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser  
20 25 30  
Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val  
35 40 45  
His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
50 55 60  
Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
65 70 75  
Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
80 85 90  
Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
95 100 105  
Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
110 115 120  
Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg  
125 130 135  
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys  
140 145 150  
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp  
155 160 165  
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala  
170 175 180  
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly  
185 190 195  
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu  
200 205 210  
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser  
215 220 225  
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu  
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro  
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala  
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser  
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu  
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser  
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala  
320 325 330

Glu Pro Glu Glu Gln  
335

<210> 34  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct

<400> 34  
tgtcctttgt cccagacttc tgtcc 25

<210> 35  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 35  
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

<210> 36  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 37  
ggcgagccct aactatccag gag 23

B1  
<210> 38  
<211> 39  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-39  
<223> Synthetic construct.

<400> 38  
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 39  
ctgctgcaaa gcgagcctct tg 22

<210> 40  
<211> 2084  
<212> DNA  
<213> Homo sapiens

<400> 40  
ggttcctggg cgctctgtta cacaagcaag atacagccag cccaccta 50  
ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100  
ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150  
tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200  
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250  
caatctattc ttgccacatc aagggtattgt tattccttta aaaaaaacc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350  
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400  
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaacttc aaggcgagtc attcccctcc tttgaatcta 550  
ccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650  
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgcccat ctcagcacat cccaatgcta cacctgctct 750  
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800  
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850  
ccatctgtga ccccttgat agtggaacca agtggaatggc ttaccacaaa 900  
cagtgatagc ttcactgggt ttaccctta tcaagaaaaa acaactctac 950  
agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000  
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050  
aggtgctatt ctgggtgtct cattgcttac tcttggtggc tacttgttgt 1100  
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agaaatgaac cagttctgcy attagacaat gcaccggaac cttatgatgt 1200  
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tgtatttttag tagtattttc ttagtagaaa atatttggtg aatcagataa 1600  
aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650  
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tgccctgaagc cctagtacca taattcaaga ttgcattttc ttaaatgaaa 1750



attgaaaggg tgcttttttaa agaaaatttg acttaaagct aaaaagagga 1800  
catagcccag agtttctggtt attgggaaat tgaggcaata gaaatgacag 1850  
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900  
gcccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000  
aagggttttg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050  
ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41

Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
1 5 10 15  
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn  
20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu  
 200 205 210  
 Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn  
 215 220 225  
 Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe  
 230 235 240  
 Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu  
 245 250 255  
 Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser  
 260 265 270  
 His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu  
 275 280 285  
 Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser  
 290 295 300  
 Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu  
 305 310 315  
 Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu  
 320 325 330

Arg Thr Ser Val

<210> 42  
 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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 gccttaccgc gcagcccga gattcactat ggtgaaaatc gccttcaata 100  
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagaçgt ggaggccctc 150  
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300  
 tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350  
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400  
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500  
 tattcatgac tttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600  
 aatctggtag agctctttgg caaactggcg agtggcagat atctgcetca 650  
 aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700  
 ttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtcc 750  
 ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800  
 tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900  
 agaagtcaga gatttacaat atgactttaa cattaagggt tatgggatac 950  
 tcaagatatt tactcatgca tttactctat tgcttatgct ttaaaaaaag 1000  
 gaaaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050  
 taattggcat tgcttggttt ttgaaactga aattacatga gtttcatttt 1100  
 ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150  
 cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200  
 tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250  
 tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300  
 tatcagatct caacattggt gggttctttt gtttttcatt ttgtacaact 1350  
 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400  
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500  
 tgtgtagggt ctgaatgctg taaggagttt aggttgatg aattctacaa 1550  
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43  
 <211> 263  
 <212> PRT  
 <213> Homo sapiens

<400> 43  
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu  
 1 5 10 15  
 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg  
 20 25 30  
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
 35 40 45  
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

	50		55		60
Ser Phe Ile Leu	Ala 65	Gly Leu Ile Val	Gly 70	Gly Ala Cys Ile	Tyr 75
Lys Tyr Phe Met	Pro 80	Lys Ser Thr Ile	Tyr 85	Arg Gly Glu Met	Cys 90
Phe Phe Asp Ser	Glu 95	Asp Pro Ala Asn	Ser 100	Leu Arg Gly Gly	Glu 105
Pro Asn Phe Leu	Pro 110	Val Thr Glu Glu	Ala 115	Asp Ile Arg Glu	Asp 120
Asp Asn Ile Ala	Ile 125	Ile Asp Val Pro	Val 130	Pro Ser Phe Ser	Asp 135
Ser Asp Pro Ala	Ala 140	Ile Ile His Asp	Phe 145	Glu Lys Gly Met	Thr 150
Ala Tyr Leu Asp	Leu 155	Leu Leu Gly Asn	Cys 160	Tyr Leu Met Pro	Leu 165
Asn Thr Ser Ile	Val 170	Met Pro Pro Lys	Asn 175	Leu Val Glu Leu	Phe 180
Gly Lys Leu Ala	Ser 185	Gly Arg Tyr Leu	Pro 190	Gln Thr Tyr Val	Val 195
Arg Glu Asp Leu	Val 200	Ala Val Glu Glu	Ile 205	Arg Asp Val Ser	Asn 210
Leu Gly Ile Phe	Ile 215	Tyr Gln Leu Cys	Asn 220	Asn Arg Lys Ser	Phe 225
Arg Leu Arg Arg	Arg 230	Asp Leu Leu Leu	Gly 235	Phe Asn Lys Arg	Ala 240
Ile Asp Lys Cys	Trp 245	Lys Ile Arg His	Phe 250	Pro Asn Glu Phe	Ile 255
Val Glu Thr Lys	Ile 260	Cys Gln Glu			

<210> 44  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 44  
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 45  
gggaactgct atctgatgcc 20

<210> 46  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 46  
caggatctcc tcttgcatgc tgcagc 26

<210> 47  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 47  
cttctcgaac cacataagtt tgaggcag 28

<210> 48  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 48  
cacgattccc tccacagcaa ctggg 25

<210> 49  
<211> 1969  
<212> DNA  
<213> Homo sapiens

<400> 49  
ggaggagggg gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100  
 cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150  
 gtttcggcgg cagccccag cctcctcadc cttctgttgc tgctgctggg 200  
 gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250  
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300  
 ccgagcctcc cgccaccctg gaccccgcc ctcagcccca catcgatggg 350  
 gccccagccc acaaccctgg ggggcccadc accccccacc aacttcctgg 400  
 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450  
 ggctccctgg cctttctgct gatgttcadc gtctgtgccg cggtcadcac 500  
 ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550  
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600  
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650  
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 cccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750  
 ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800  
 agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850  
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900  
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 tccccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000  
 agtcctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050  
 ccccggtgat gaaaaggcct tcagccctga ctgcttcctg aactccctc 1100  
 cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150  
 cagaaatgct ggtccccggt gcccggagg aatcttacca agtgccatca 1200  
 tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250  
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300  
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350  
 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400  
 aatactgtc ttaattttcc tgaagggtggc cccctgtttc tagttggtcc 1450  
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550  
 gatcagggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600  
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650  
 ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700  
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750  
 gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800  
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950  
 aaaaaaaaaa aaaaaaaga 1969

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	20	25	30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	35	40	45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	50	55	60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly	65	70	75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	80	85	90	
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	95	100	105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	110	115	120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	125	130	135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	140	145	150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	155	160	165	

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr  
 170 175 180  
 Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp  
 185 190 195  
 Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys  
 200 205 210  
 Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro  
 215 220 225  
 Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu  
 230 235 240  
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly  
 245 250 255  
 Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro  
 260 265 270  
 Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val  
 275 280

<210> 51  
 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50  
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100  
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150  
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200  
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250  
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300  
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350  
 caaagaggcc ggaggggag ctggctctaa agtcagttag gcccttggcc 400  
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450  
 ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500  
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550  
 acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600  
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaagggtg 650  
 ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700



tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750  
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 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850  
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900  
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950  
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000  
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050  
 agtgggtggca gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100  
 tgagtcctcc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150  
 ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200  
 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250  
 agtttccagc aacatgaggg aaataagcaa agagggaat cgcctccttg 1300  
 gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350  
 ggaggtgacg ctggttggtg agtcaatact gtgaactctg agacgtctcc 1400  
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450  
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500  
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550  
 ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52  
 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys  
 1 5 10 15  
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser  
 20 25 30  
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
 35 40 45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50 55 60  
 Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr  
 65 70 75  
 Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly  
 80 85 90  
 Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala  
 95 100 105  
 Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val  
 110 115 120  
 Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val  
 125 130 135  
 Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile  
 140 145 150  
 Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro  
 155 160 165  
 Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser  
 170 175 180  
 Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln  
 185 190 195  
 Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly  
 200 205 210  
 Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln  
 215 220 225  
 Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly  
 230 235 240  
 Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser  
 245 250 255  
 Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly  
 260 265 270  
 Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser  
 275 280 285  
 Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser  
 290 295 300  
 Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly  
 305 310 315  
 Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His  
 320 325 330  
 Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly  
 335 340 345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn  
 350 355 360  
 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser  
 365 370 375  
 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly  
 380 385 390  
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser  
 395 400 405  
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
 410 415 420  
 Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg  
 425 430 435  
 Ser Ser Arg Ile Pro  
 440

<210> 53  
 <211> 3580  
 <212> DNA  
 <213> Homo sapiens

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 <213> Homo sapiens

<400> 54

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Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser  
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Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys  
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215 220 225  
Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp  
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 <212> PRT  
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 Val Ser Pro Gly Arg Met Arg Gln Phe Asp Asp Leu Phe Arg Gly  
 185 190 195  
 Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr  
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 <212> DNA  
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<400> 57

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<212> PRT  
 <213> Homo sapiens

<400> 58

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 50 55 60  
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu  
 65 70 75  
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr  
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 Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln  
 95 100 105  
 Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala  
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 Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln  
 125 130 135  
 His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys  
 140 145 150  
 His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val  
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 Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met  
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 Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile  
 230 235 240  
 Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser  
 245 250 255  
 Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser  
 260 265 270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu  
 275 280 285  
 Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met  
 290 295 300  
 Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr  
 305 310 315  
 Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser  
 320 325 330  
 Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu  
 335 340 345  
 Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala  
 350 355 360  
 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala  
 365 370 375  
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln  
 380 385 390  
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln  
 395 400 405  
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp  
 410 415 420  
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu  
 425 430 435  
 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg  
 440 445 450  
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu  
 455 460 465  
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser  
 470 475 480  
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro  
 485 490 495  
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val  
 500 505 510  
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile  
 515 520 525  
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu  
 530 535 540  
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys  
 545 550 555  
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560 565 570  
 Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln  
 575 580 585  
 Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp  
 590 595 600  
 His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile  
 605 610 615  
 Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg  
 620 625 630  
 Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys  
 635 640 645  
 Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile  
 650 655 660  
 Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly  
 665 670 675  
 Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu  
 680 685 690  
 Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr  
 695 700 705  
 Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr  
 710 715 720  
 Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met  
 725 730 735  
 Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr  
 740 745 750  
 Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys  
 755 760 765  
 Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His  
 770 775 780  
 Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn  
 785 790 795  
 Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr  
 800 805 810  
 Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro  
 815 820 825  
 Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg  
 830 835 840  
 Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro  
 845 850 855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile  
 860 865 870  
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln  
 875 880 885  
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro  
 890 895 900  
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His  
 905 910 915  
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala  
 920 925 930  
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala  
 935 940 945  
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu  
 950 955 960  
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His  
 965 970 975  
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly  
 980 985 990  
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro  
 995 1000 1005  
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys  
 1010 1015 1020  
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg  
 1025 1030 1035  
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro  
 1040 1045 1050  
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu  
 1055 1060 1065  
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp  
 1070 1075 1080  
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly  
 1085 1090 1095  
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr  
 1100 1105 1110  
 Pro Pro Leu Thr Ile  
 1115

<210> 59  
 <211> 25  
 <212> DNA  
 <213> Artificial



<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 59  
gggaaacaca gcagtcattg cctgc 25

<210> 60  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 60  
gcacacgtag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-42  
<223> Synthetic construct.

<400> 61  
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
cgaggaggctg ggtcgatcatg atccggaccc cattgtcggc ctctgcccac 50  
cgctgtctcc tcccaggctc ccgcgggccga ccccgcgca acatgcagcc 100  
cacggggccgc gaggggttccc gcgcgctcag ccggcggtat ctgcggcgctc 150  
tgctgtctct gctactgctg ctgctgctgc ggcagcccggt aaccgcgcgcg 200  
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccacg 250  
cctcttcacc acgcccgggtg tccccagcgc cctcactacc ccaggcctca 300  
ctacgccagg ccccccaaa accctggacc ttgggggtcg cgcgcaggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400  
 cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
 tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500  
 gcccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
 cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
 cctactctga actcgagctt gtgacctcag ctgaaggtct gaacagctct 650  
 caaaagctgg cctgcctcat tggcgtgnag ggtgggtcact cactggacag 700  
 cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750  
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 agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850  
 agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900  
 catcggacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950  
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000  
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtga 1050  
 cactgtccat ggggggtgctg cagtgcgaacc tgcttgctaa cgtgtccact 1100  
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150  
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 aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250  
 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300  
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350  
 tggaggctga gtttccatat gggcaactga gcacatcctg cactcccac 1400  
 ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
 gccaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500  
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550  
 tgctgacaca gtcggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600  
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
 cacatggaaa a 1661

<210> 63  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63

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 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg  
 20 25 30  
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala  
 35 40 45  
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
 50 55 60  
 Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro  
 65 70 75  
 Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser  
 80 85 90  
 Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg  
 95 100 105  
 Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe  
 110 115 120  
 Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val  
 125 130 135  
 Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp  
 140 145 150  
 Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His  
 155 160 165  
 Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala  
 170 175 180  
 Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val  
 185 190 195  
 Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser  
 200 205 210  
 Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys  
 215 220 225  
 Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met  
 230 235 240  
 Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val  
 245 250 255  
 Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala

260 265 270  
 Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro  
 275 280 285  
 Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu  
 290 295 300  
 Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly  
 305 310 315  
 Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu  
 320 325 330  
 Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg  
 335 340 345  
 Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp  
 350 355 360  
 Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr  
 365 370 375  
 Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu  
 380 385 390  
 Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg  
 395 400 405  
 Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val  
 410 415 420  
 Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser  
 425 430 435  
 His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val  
 440 445 450  
 Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala  
 455 460 465  
 Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro  
 470 475 480  
 Thr Phe Thr Gln Trp Leu Cys  
 485

<210> 64  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 65  
gtcacacaca gctctggcag ctgag 25

<210> 66  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 66  
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67  
<211> 1564  
<212> DNA  
<213> Homo sapiens

<400> 67  
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50  
aacaccacaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100  
ggcccagcaa gcctgataag catgaagctc ttatcttttg tggctgtggt 150  
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200  
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250  
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450  
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650  
atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
ctccttctcc ctaacttttag aaatgttgta cttggctatt ttgattaggg 850  
aagaggggatg tggctctctga tctctgttgt cttcttgggt ctttgggggt 900  
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950  
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
cagctctgag tcttgggaat gttgttacc ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100  
gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150  
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tgggccccct gagccactg ggtcttcagg gtgcactgga agctgggtgt 1250  
cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300  
ctctgctgcc ggtccccctca cctgcacttg aggggtcttg gcagtccctc 1350  
ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450  
gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550  
ttttatttct ctca 1564

<210> 68  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 68  
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
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Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
20 25 30  
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
35 40 45  
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
 65 70 75  
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
 80 85 90  
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
 95 100 105  
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
 110 115 120  
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
 125 130 135  
 Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
 140 145 150  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
 155 160 165  
 Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
 170 175 180  
 Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
 agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50  
 agttcatagg gtctgggttc cccgaaccag gaagggttga gggaacacaa 100  
 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggctctccc 150  
 tccctttgca ttcccacccc tccgggcttt gcgtcttctt ggggaccccc 200  
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250  
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300  
 tcgcgggcca aactcaactc catcaagtcc tctctggggc gggagacgcc 350  
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550  
 gcatgtgctg cccagtagcc cgctgcaata atggcatctg tatcccagtt 600  
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700  
 atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
 gacccttgcc tacgatcatc agactgcatt gaaggggttt gctgtgctcg 800  
 tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850  
 gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900  
 tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950  
 ctctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
 ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050  
 catgggtggaa aataagggtc agatgcagaa gaatggctaa aataagaaac 1100  
 gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
 aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
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 agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
 aagagtttag gttgtgctgg aggagagggt tccttcagat tgctgattgc 1350  
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 aaaatactcc tagaataact tggtatacaa taggttctaa aaataaaatt 1450  
 gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
 taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550  
 agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
 cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650  
 ccacaaatac ttttttttca aaattttagt ttacctgta attaataaga 1700  
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 aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850  
 ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900  
 gctaacagag agatcattat ttcttaaaga ttggccataa cctatatattt 1950  
 gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000  
 agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050  
 aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

B1



aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150  
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 tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250  
 tgctgagatc ctcaaataat ctcaatttca ggaggtttca caaatgtac 2300  
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 accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550  
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 agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
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 caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850  
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 atataacaat tatttatattt acaatttggt ttctgcaata tttttcttat 2950  
 gtccaccctt ttaaaaatta ttatttgaag taatttatatt acaggaaatg 3000  
 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
 gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
 taagataaaa tctattaaat ttttctctc taaaaactga aaaaaaaaaa 3150  
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70  
 <211> 259  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
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 Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
 20 25 30  
 Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
 35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
 50 55 60  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
 65 70 75  
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
 80 85 90  
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
 95 100 105  
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
 110 115 120  
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
 125 130 135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
 140 145 150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
 155 160 165  
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
 170 175 180  
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
 185 190 195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
 200 205 210  
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
 215 220 225  
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
 230 235 240  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
 245 250 255  
 Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100  
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250  
 atatttttagt aattcatatg ttttagatta taggttttaa catacttggtg 300  
 aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350  
 ggatttggtc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400  
 tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
 tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550  
 ctcaagcccc caacatccca gtcctcagtc ctcagtcac ttgacttcaa 600  
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
 agcaccagag ccaggcagtc actgttctc ctcttggttt ggagtccttt 700  
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
 tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800  
 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
 atacccccag cttctaagat cccagcttct gcagtggaaa tgcctggttc 900  
 agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950  
 cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000  
 aatcagattc ccatcagctt gtattogaag tctttaagtg agcctttgaa 1050  
 tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100  
 ccgtcattac ctctgcagtc ctgacaagct catcactgaa ttctgctagt 1150  
 ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200  
 cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250  
 tgaatggaca tgggtggtggt cgaagtcagc agacactaga cagtaagtat 1300  
 agcagcaagc tactcttgtc atggctggtg ccaaccaaac agaggaagag 1350  
 gatagctcac gtgatgtgga aaacaccagt tggatcaatgg ctcatcgtt 1400  
 aaaaagcagc ccttttgctt ttttggtttt ggaccaggtg ttggctgtgg 1450  
 tgttattaga aatgtcttaa ccacagcaag aaggaggtgg tggctctcata 1500  
 ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550  
 tttaaagatg cttgggccag gcgggggtggc tgatgccccat aatcccagtg 1600  
 ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750  
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
ctgaaaaga 1809

<210> 72  
<211> 363  
<212> PRT  
<213> Homo sapiens

<400> 72

Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile  
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Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly  
20 25 30  
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys  
 230 235 240  
 Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala  
 245 250 255  
 Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser  
 260 265 270  
 Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser  
 275 280 285  
 Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln  
 290 295 300  
 Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn  
 305 310 315  
 Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr  
 320 325 330  
 Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg  
 335 340 345  
 Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp  
 350 355 360

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 73  
 aattcatggc aaatatttcc cttccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 74  
 tggtaaactg gcccaaactc gg 22

<210> 75  
 <211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

B1

<400> 76  
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tgactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagggt 200  
caccgacggc cccccggcca cccccgccta ctgggacggc gagaaggagg 250  
tgctggcggg ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300  
gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtgggtgca 350  
ctgggaccgg cagccgcccc gggccccgca cgaccgcgcg gaccgcctgc 400  
tggaacctta cgcgtcgggc gagcgcgcgc cctacgggcc cttttttctg 450  
cgcgaccgcg tggctgtggg cgcggatgcc tttgagcgcg gtgacttctc 500  
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cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700  
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750  
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cagaacttgg cagccttgaa gttgggtgca gcctcggcag gactccact 1550  
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tggctgagga caggggaggg agtgaagttg gtttgggtg gcctgtgttg 1900  
ccactctcag cccccacat ttgcatctgc tgggtggacct gccaccatca 1950  
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989

<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu  
1 5 10 15  
Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp  
20 25 30  
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His  
 80 85 90  
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His  
 95 100 105  
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg  
 110 115 120  
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro  
 125 130 135  
 Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu  
 140 145 150  
 Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp  
 155 160 165  
 Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu  
 170 175 180  
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala  
 185 190 195  
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser  
 200 205 210  
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val  
 215 220 225  
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln  
 230 235 240  
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu  
 245 250 255  
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu  
 260 265 270  
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn  
 275 280 285  
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg  
 290 295 300  
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu  
 305 310 315  
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp  
 320 325 330  
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys  
 335 340

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens



<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150  
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250  
cactgccaag gagtactgga tgttcaaact ccgcaactcc tccagcccag 300  
ccaccgggga ggaccctgag ggctcagaca tctgaacta ctttgagagc 350  
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cttctgctt gtcaacaggg ttgcagtcca catcgtgtc ctggcctcac 450  
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tatgtgtgct tgggcttaac actgggctca gcctgctcta ccctcctggg 1450

gcacctcatc tagaagggag gacacaagga cattggtgct tcagagcctt 1500  
tgaagatgag aagagagtgc aggagggctg ggggccatgg aggaaaggcc 1550  
taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1600  
ccaagatgc cagtgagcca cgtccatgcc cattccgtgc aaggcagata 1650  
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gccagtgcc aaaccagcc atgggctctt tgcaacctcc cagctgcgct 1850  
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ccactaacca gactggaaaa ccagaaaaga tgggccttcc atgaatgctt 2050  
cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100  
ggcctggggt ttcaaaaaaa gagggatcct catgacctgg tggcttatgg 2150  
cctgggtcaa gatgaggggc tttcagtgtt cctgtttaca acatgtcaaa 2200  
gccattgggt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79  
<211> 475  
<212> PRT  
<213> Homo sapiens

<400> 79  
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser  
1 5 10 15  
Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala  
20 25 30  
Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg  
35 40 45  
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
50 55 60  
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
65 70 75  
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
80 85 90  
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val  
 110 115 120  
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val  
 125 130 135  
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr  
 140 145 150  
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe  
 155 160 165  
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr  
 170 175 180  
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met  
 185 190 195  
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr  
 200 205 210  
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp  
 215 220 225  
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe  
 230 235 240  
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu  
 245 250 255  
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe  
 260 265 270  
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser  
 275 280 285  
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro  
 290 295 300  
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val  
 305 310 315  
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile  
 320 325 330  
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe  
 335 340 345  
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu  
 350 355 360  
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn  
 365 370 375  
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile  
 380 385 390  
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395 400 405  
 Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser  
 410 415 420  
 Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu  
 425 430 435  
 Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly  
 440 445 450  
 Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser  
 455 460 465  
 Ala Cys Ser Thr Leu Leu Val His Leu Ile  
 470 475

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 80  
 ttttgcggtc accattgtct gc 22

<210> 81  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 81  
 cgtaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-49  
 <223> Synthetic construct.

<400> 82  
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844

<212> DNA  
<213> Homo sapiens

<400> 83

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ctggagacac catctccac cgagagtcac ggccccattg gccctgcacc 100  
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ctatgagcag ctgctcaagg tggtagcctg ggggctcaat cggaccctga 250  
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cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
tggtaggaga ggtgcccagag aagctgggct acgccttgcg tccccaggaa 600  
aagggccact cgcccgaaga catctaccag atggctctca accaggccct 650  
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700  
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cgcgctgctg ctggcctcgt acacgtggtc ggacgcggcg gcagcgttcg 1300  
ccggcttgag ccgggaagag gcgttgcgct tggcgctcga cgacgtggcg 1350

gcattgcacg ggcctgtcgt gcgccagctc tgggacggca ccggcgtcgt 1400  
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 cgcattctact ttgccggcga gcacaccgcc taccgcgacg gctgggtgga 1550  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu  
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 20 25 30  
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195  
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr  
 200 205 210  
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala  
 215 220 225  
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr  
 230 235 240  
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp  
 245 250 255  
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro  
 260 265 270  
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala  
 275 280 285  
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln  
 290 295 300  
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala  
 305 310 315  
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile  
 320 325 330  
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg  
 335 340 345  
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg  
 350 355 360  
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn  
 365 370 375  
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu  
 380 385 390  
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala  
 395 400 405  
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu  
 410 415 420  
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp  
 425 430 435  
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser  
 440 445 450  
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu	545		550		555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His	560		565		

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 ctctgggccg gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100  
 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150  
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
 cccctcgcga gggctctgaat ttctctgctgc tgttcacaaa gatgcttttt 250  
 atctttaact ttttgttttc ccacttccg accccggcgt tgatctgcat 300  
 cctgacattt ggagctgcc tcttcttggtg gctgatcacc agacctcaac 350  
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400  
 ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450  
 cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgtctg 500  
 tgtctgacaa tgggccctgc ttgggatata gaaaaccaa ccagccctac 550  
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600  
 ctgtctcttg cataaagggt ataatcatc accagaccag tttgtcggca 650  
 tctttgctca gaataggcca gagtggatca tctccgaatt ggcttggttac 700  
 acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750



catcgtacat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800  
caccccaaaa ggcattggtg ctgatagga atgtagagaa aggcttcacc 850  
ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900  
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950  
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000  
gacctgagcg tcactgtctt caccagtggg accacaggtg accccaaagg 1050  
agccatgata acccatcaaa atattgtttc aaatgctgct gcctttctca 1100  
aatgtgtgga gcatgcttat gagcccactc ctgatgatgt ggccatatcc 1150  
tacctccctc tggctcatat gtttgagagg attgtacagg ctgttggtga 1200  
cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250  
ctgacgacat gaagactttg aagcccacat tgtttcccgc ggtgcctcga 1300  
ctccttaaca ggatctacga taaggtacaa aatgaggcca agacaccctt 1350  
gaagaagttc ttgttgaagc tggctgtttc cagtaaattc aaagagcttc 1400  
aaaagggtat catcaggcat gatagtttct gggacaagct catctttgca 1450  
aagatccagg acagcctggg cggaagggtt cgtgtaattg tcaactggagc 1500  
tgcccccatg tccacttcag tcatgacatt cttccgggca gcaatgggat 1550  
gtcaggtgta tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600  
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ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700  
tgaataatga aggagaggtc tgcacaaagg gtacaaacgt gttcaaagga 1750  
tacctgaagg accctgagaa gacacaggaa gccctggaga gtgatggctg 1800  
gcttcacaca ggagacattg gtcgctggct cccgaatgga actctgaaga 1850  
tcatcgaccg taaaaagaac attttcaagc tggcccaagg agaatacatt 1900  
gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950  
aatTTTTgta cacggggaga gcttacggtc atccttagta ggagtgggtg 2000  
ttcctgacac agatgtactt ccctcatttg cagccaagct tggggtgaag 2050  
ggctcctttg aggaactgtg ccaaaaccaa gttgtaaggg aagccatttt 2100  
agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150  
aggtcaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200

ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250  
 tcggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300  
 tacttaagta cctgccggcc cactgtgcac tgcttgtgag aaaatggatt 2350  
 aaaaactatt cttacatttg ttttgccttt cctcctattt ttttttaacc 2400  
 tgttaaactc taaagccata gcttttgttt tatattgaga catataatgt 2450  
 gtaaacttag ttcccaaata aatcaatcct gtctttccca tcttcgatgt 2500  
 tgctaataatt aaggcttcag ggctactttt atcaacatgc ctgtcttcaa 2550  
 gatcccagtt tatgttctgt gtccttcctc atgatttcca accttaatac 2600  
 tattagtaac cacaagttca aggggtcaaag ggaccctctg tgccttcttc 2650  
 tttgttttgt gataaacata acttgccaac agtctctatg cttatttaca 2700  
 tcttctactg ttcaaactaa gagattttta aattctgaaa aactgcttac 2750  
 aattcatgtt ttctagccac tccacaaacc actaaaattt tagtttttagc 2800  
 ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctctt 2850  
 ctgcgtaaatt taaattgtgt actgaaggga aaagtttgat cataccaaac 2900  
 atttctctaaa ctctctagtt agatatctga cttggggagta ttaaaaattg 2950  
 ggtctatgac atactgtcca aaaggaatgc tgttcttaaa gcattattta 3000  
 cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050  
 gaagctgtgg gggaaggagt tgacaggtgg gccagtgaa cttttccagt 3100  
 aatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150  
 acaggcaagc aagatgcccc cacaacaggc ttattttctg tgaaggaacc 3200  
 aactgatctc cccaccctt ggattagagt tctgtctcta ccttaccac 3250  
 agataacaca tgttgtttct acttgtaaatt gtaaagtctt taaaataaac 3300  
 tattacagat aaaaaa 3316

<210> 86  
 <211> 739  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
 Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg  
 1 5 10 15  
 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro  
 20 25 30

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser  
 35 40 45  
 Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile  
 50 55 60  
 Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys  
 65 70 75  
 Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg  
 80 85 90  
 Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val  
 95 100 105  
 Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn  
 110 115 120  
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu  
 125 130 135  
 Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu  
 140 145 150  
 Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys  
 155 160 165  
 Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His  
 170 175 180  
 Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala  
 185 190 195  
 Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr  
 200 205 210  
 Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu  
 215 220 225  
 Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile  
 230 235 240  
 Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu  
 245 250 255  
 Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro  
 260 265 270  
 Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu  
 275 280 285  
 Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe  
 290 295 300  
 Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys  
 305 310 315  
 Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr

320 325 330  
 His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val  
 335 340 345  
 Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr  
 350 355 360  
 Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val  
 365 370 375  
 Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg  
 380 385 390  
 Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro  
 395 400 405  
 Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn  
 410 415 420  
 Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val  
 425 430 435  
 Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp  
 440 445 450  
 Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu  
 455 460 465  
 Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser  
 470 475 480  
 Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val  
 485 490 495  
 Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe  
 500 505 510  
 Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu  
 515 520 525  
 Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr  
 530 535 540  
 Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn  
 545 550 555  
 Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala  
 560 565 570  
 Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp  
 575 580 585  
 Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile  
 590 595 600  
 Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu  
 605 610 615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His  
 620 625 630  
 Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp  
 635 640 645  
 Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly  
 650 655 660  
 Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile  
 665 670 675  
 Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr  
 680 685 690  
 Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser  
 695 700 705  
 Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly  
 710 715 720  
 Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu  
 725 730 735  
 His Ile Gln Asp

<210> 87  
 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
 ggagggcggag gccgcggcga gccggggccga gcagtgaggg ccctagcggg 50  
 gcccgagcgg ggcccggggc ccctaagcca ttctgaagt catgggctgg 100  
 ccaggacatt ggtgacccgc caatccggta tggacgactg gaagcccagc 150  
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200  
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250  
 cagggggccgt gcttttcctg ctggtgactg tcattgtcaa tatcaagttg 300  
 atcctggaca ctgcggcagc catcagtga gccaatgaag acccagagcc 350  
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400  
 gaggcagtgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc 450  
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500  
 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550  
 gccacgtgat ggcaaacgt gtgtttgaca cgtactcacc tcatgaggat 600  
 gaggccatgg tgctattcct caacatggta gcgcccggcc gagtgctcat 650

ctgcactgtc aaggatgagg gctccttcca cctcaaggac acagccaagg 700  
 ctctgctgag gagcctgggc agccaggctg gccctgccct gggctggagg 750  
 gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800  
 acattctaag tcacctgccc tctcttctctg gggggaccca gtcctgctga 850  
 agacagatgt gccattgagc tcagcagaag aggacagagt ccactgggca 900  
 gacacagagc tgaaccgtcg ccgccggcgc ttctgcagca aagttgaggg 950  
 ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000  
 ctgaccact cccagacaac aaggtcctca atgtgcctgt ggctgtcatt 1050  
 gcagggaacc gaccaatta cctgtacagg atgtgcgct ctctgctttc 1100  
 agcccagggg gtgtctctc agatgataac agttttcatt gacggctact 1150  
 atgaggaacc catggatgtg gtggcactgt ttggtctgag gggcatccag 1200  
 catactccca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250  
 cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300  
 ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350  
 caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400  
 ctggaatgac caggggtatg aacacacggc tgaggacca gcactactgt 1450  
 accgtgtgga gaccatgcct gggctgggct ggggtgctcag gaggtccttg 1500  
 tacaaggagg agcttgagcc caagtggcct acaccgaaa agctctggga 1550  
 ttgggacatg tggatgcgga tgcctgaaca acgccggggc cgagagtga 1600  
 tcatccctga cgtttcccga tcctaccact ttggcatcgt cggcctcaac 1650  
 atgaatggct actttcacga ggcctacttc aagaagcaca agttcaacac 1700  
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 agcaagaacc cttgtgaaga ctctttcctg ccagacacag agggccacac 1850  
 ctacgtggcc tttattcgaa tggagaaaga tgatgacttc accacctgga 1900  
 cccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950  
 catcggggcc tgtggagatt gtttcggaag aagaaccact tcctgggtgg 2000  
 ggggggtccc gcttccccct actcagtga gaagccaccc tcagtcaccc 2050  
 caattttcct ggagccaccc ccaaaggagg agggagcccc aggagcccca 2100

B1

gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150  
 cccccaggct ggctagccct tccctccatc ctgtaggatt ttgtagatgc 2200  
 tggtaggggc tggggctacc ttgtttttaa catgagactt aattactaac 2250  
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 ctatttattt acttccttgt tggagaaggg caggagagta cctgggaatc 2350  
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 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650  
 caaagctgga taagttgggc attgattaaa aaaggagaag ccctctggga 2700  
 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
 Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala  
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 Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr  
                   20                  25                  30  
 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu  
                   35                  40                  45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
                   50                  55                  60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
                   65                  70                  75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
                   80                  85                  90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
                   95                  100                  105  
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
                   110                  115                  120  
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
                   125                  130                  135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp  
 140 145 150  
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn  
 155 160 165  
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu  
 170 175 180  
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser  
 185 190 195  
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp  
 200 205 210  
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His  
 215 220 225  
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu  
 230 235 240  
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His  
 245 250 255  
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser  
 260 265 270  
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr  
 275 280 285  
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu  
 290 295 300  
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu  
 305 310 315  
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro  
 320 325 330  
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met  
 335 340 345  
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro  
 350 355 360  
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser  
 365 370 375  
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val  
 380 385 390  
 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe  
 395 400 405  
 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr  
 410 415 420  
 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu



	425	430	435
Asp Pro Ala Leu	Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
	440	445	450
Trp Val Leu Arg	Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
	455	460	465
Trp Pro Thr Pro	Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
	470	475	480
Met Pro Glu Gln	Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
	485	490	495
Ser Arg Ser Tyr	His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
	500	505	510
Tyr Phe His Glu	Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
	515	520	525
Pro Gly Val Gln	Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
	530	535	540
Tyr Glu Val Glu	Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
	545	550	555
Asp His Ser Lys	Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
	560	565	570
Glu Gly His Thr	Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
	575	580	585
Asp Phe Thr Thr	Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
	590	595	600
Asp Leu Asp Val	Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
	605	610	615
Arg Lys Lys Asn	His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
	620	625	630
Tyr Ser Val Lys	Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu		
	635	640	645
Pro Pro Pro Lys	Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr		
	650	655	660

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25

<210> 90  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

β1 <400> 90  
cctcaaccag gccacgggcc ac 22

<210> 91  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 91  
cccaggcaga gatgcagtac aggc 24

<210> 92  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 92  
cctccagtag gtggatggat tggctc 26

<210> 93  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 93  
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94  
<211> 3037  
<212> DNA  
<213> Homo sapiens

<400> 94

B1  
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ctcttggaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100  
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B1

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<210> 95  
 <211> 307  
 <212> PRT  
 <213> Homo sapiens

<400> 95

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 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
 35 40 45  
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
 50 55 60  
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
 65 70 75  
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
 80 85 90  
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
 95 100 105  
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
 110 115 120  
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
 125 130 135  
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
 140 145 150  
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
 155 160 165  
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
 170 175 180  
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
 185 190 195  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
 200 205 210  
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
 215 220 225  
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

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Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
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Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
				275					280					285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
				290					295					300
Leu	Ser	Val	Gly	His	Gln	His								
				305										

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 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 96  
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<210> 97  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 97  
 ctgtgctcat gttcatggac aactg 25

<210> 98  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 98  
 ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99  
 <211> 1429

<212> DNA  
<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150  
ccgcccctcg tgctggccgc cctggtggcc tgcattcatc tcttgggctt 200  
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ggggaatgaa gctgtagctt ccagagacct gaggtaaac aacgaccaga 700  
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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe  
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg  
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg  
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu  
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe  
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val  
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu  
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln  
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg  
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu  
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys  
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp  
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu  
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly  
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser  
230 235 240



Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr  
 245 250 255  
 Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu  
 260 265 270  
 Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val  
 275 280 285  
 Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro  
 290 295 300  
 Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met  
 305 310 315  
 Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu  
 320 325 330  
 Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu  
 335 340 345  
 Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser  
 350 355 360  
 Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile  
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<210> 101  
 <211> 3671  
 <212> DNA  
 <213> Homo sapiens

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<210> 102  
 <211> 1089  
 <212> PRT  
 <213> Homo sapiens

<400> 102

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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro  
 35 40 45  
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala  
 50 55 60  
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile  
 65 70 75  
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val  
 80 85 90  
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser  
 95 100 105  
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu  
 110 115 120  
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu  
 125 130 135  
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly  
 140 145 150  
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys  
 155 160 165  
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp  
 170 175 180  
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe  
 185 190 195  
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

200 205 210  
 Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp  
 215 220 225  
 Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys  
 230 235 240  
 His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met  
 245 250 255  
 Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr  
 260 265 270  
 Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp  
 275 280 285  
 His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu  
 290 295 300  
 Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro  
 305 310 315  
 Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu  
 320 325 330  
 Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala  
 335 340 345  
 Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala  
 350 355 360  
 Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser  
 365 370 375  
 Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala  
 380 385 390  
 Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala  
 395 400 405  
 Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr  
 410 415 420  
 Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala  
 425 430 435  
 Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg  
 440 445 450  
 Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys  
 455 460 465  
 Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys  
 470 475 480  
 Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile  
 485 490 495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu  
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe  
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala  
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Phe  
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala  
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val  
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu  
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg  
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu  
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr  
635 640 645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met  
650 655 660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala  
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg  
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg  
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala  
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu  
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu  
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val  
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu  
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785 790 795  
 Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly  
 800 805 810  
 Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala  
 815 820 825  
 Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu  
 830 835 840  
 Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile  
 845 850 855  
 Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu  
 860 865 870  
 His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe  
 875 880 885  
 Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr  
 890 895 900  
 Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile  
 905 910 915  
 His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser  
 920 925 930  
 Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala  
 935 940 945  
 Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp  
 950 955 960  
 Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro  
 965 970 975  
 Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu  
 980 985 990  
 Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe  
 995 1000 1005  
 Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu  
 1010 1015 1020  
 Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg  
 1025 1030 1035  
 Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe  
 1040 1045 1050  
 Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly  
 1055 1060 1065  
 Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe  
 1070 1075 1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

B1  
<400> 103  
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gcagttccct gtgtctctgg tggtttgcct aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150  
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300  
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350  
taaatacaaac agaacgtggt ccagtggtgt gaccaaccac acgctgggtgc 400  
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450  
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550  
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600  
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750  
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800  
ccttaatgat cctcagccca gcgggaacct gagggcccct caggaggaag 850  
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950  
cagcagaaca ataccccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050  
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggtt 1100  
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccc 1200  
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250



gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300  
 agccttctga gggggatggg ctcggagagg agggctcttct atctagactc 1350  
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400  
 catgcaattc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450  
 gccaacactt ccttttgcct tttgtttcct gtgcaaaca gtgagtcacc 1500  
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550  
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 cgtgtgtgat tggttcatgc atgtaggtct cttaacaatg atggtgggcc 1650  
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcagt 1700  
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104  
 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
 Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys  
 1 5 10 15  
 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu  
 20 25 30  
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr  
 35 40 45  
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser  
 50 55 60  
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu  
 65 70 75  
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His  
 80 85 90  
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val  
 95 100 105  
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro  
 110 115 120  
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu  
 125 130 135  
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile  
 140 145 150  
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr  
 155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile  
 170 175 180  
 Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys  
 185 190 195  
 Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys  
 200 205 210  
 Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val  
 215 220 225  
 Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro  
 230 235 240  
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu  
 245 250 255  
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser  
 260 265 270  
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys  
 275 280 285  
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys  
 290 295 300  
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser  
 305 310 315  
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu  
 320 325 330  
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp  
 335 340 345  
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro  
 350 355 360  
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr  
 365 370 375  
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
 380 385 390  
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
 395 400 405  
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
 410 415 420  
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
 425 430 435  
 Leu Tyr Val Gln Met Glu Asn  
 440

<210> 105

<211> 21  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct  
  
<400> 105  
cgctgctgct gttgctcctg g 21

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial

B1  
<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 106  
cagtgtgccca ggactttg 18

<210> 107  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 107  
agtcgcaggc agcgttgg 18

<210> 108  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 108  
ctcctccgag tctgtgtgct cctgc 25

<210> 109  
<211> 51  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctgggtgt ttgcctaaac ctgcaaacaat 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

B1  
<400> 110  
cggacgcgtg ggcggacgcg tgggcggacg cgtgggtctc tgcggggaga 50  
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100  
tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150  
gctcctgggg ggcccagatc atcggggggc acgaggtgac cccccactcc 200  
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250  
cttctgctg cgagcccgt ggggtggtctc ggccgcccac tgcttcagcc 300  
acagagacct ccgcactggc ctggtggtgc tgggcgcca cgtcctgagt 350  
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccocatga cccacgcca cgacatctgc ctgctgcggc 450  
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500  
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ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600  
ccaaggtccg agtgtggac ccggacgtct gcaacagctc ctggaagggc 650  
cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700  
gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750  
ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800  
cccgacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850  
ggttcggcgg agcagtcacc agcccggccc cctgcctggg accaccaggc 900  
ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000  
tggttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
1 5 10 15  
Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
20 25 30  
Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
35 40 45  
Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
50 55 60  
Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
65 70 75  
Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
80 85 90  
His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
95 100 105  
Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
110 115 120  
Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
125 130 135  
Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
140 145 150  
Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
155 160 165  
Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
170 175 180  
Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
185 190 195  
Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg  
200 205 210  
Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg  
215 220 225  
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly  
230 235 240  
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val  
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
275 280

<210> 112  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 112  
gacgtctgca acagctcctg gaag 24

B1  
<210> 113  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 113  
cgagaaggaa acgaggccgt gag 23

<210> 114  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 114  
tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115  
<211> 1808  
<212> DNA  
<213> Homo sapiens

<400> 115  
gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50  
cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggatcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250  
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
 tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400  
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450  
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500  
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550  
 tgctggacaa gctgaaagcc tcagcccctt cgcgatcat caacctctcg 600  
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650  
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 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750  
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800  
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 ggaggctttg ggctgaaagt gcccgccctg tgggcttaga ggctccctct 1050  
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 ctggcactac ctgagccggg agaccagga ctggcgccg ccatgcccgc 1200  
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250  
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 agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350  
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 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450  
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 ctgtctccca tgatggtgtg gtacagcgag ctgttgctg gctatggcat 1600  
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gagagcaggt gcaggtgtca tcccagattc aggctctgca cggcatggag 1700  
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
 gctcattt 1808

<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116

Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
 1 5 10 15  
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
 20 25 30  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
 35 40 45  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
 50 55 60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
 65 70 75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
 80 85 90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
 95 100 105  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
 110 115 120  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
 125 130 135  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
 140 145 150  
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
 155 160 165  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
 170 175 180  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
 185 190 195  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
 200 205 210  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
 215 220 225



Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His  
 230 235 240  
 Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro  
 245 250 255  
 Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro  
 260 265 270  
 Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly  
 275 280 285  
 Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala  
 290 295 300  
 Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg  
 305 310 315  
 Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro  
 320 325 330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgctggca tgtggctcctg gggcgcggtt ggcggcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgccccg 150  
 agcgccgggt gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200  
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450  
 aggacgtgta catgctcaat gtgaaaggcc tggcccaggg tgtctttcag 500  
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 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
 cgtgtgccct cagcctctct cgggagtctt ttctctacag cccagataat 800  
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 cccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000  
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050  
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
 ggctgaagga cactgttgac ccaaaactgg tgaccctcaa ccaccgcatt 1250  
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450  
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 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
 actgaactgt tggcagagag aagctgggtg agtcctgtgg ctttccagag 1700  
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
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 ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950  
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000  
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
 tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100  
 agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala  
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Arg Gly Asp Thr  
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg  
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala  
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu  
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe  
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His  
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr  
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly  
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn  
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser  
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr  
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly  
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu  
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser  
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala  
230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu  
 245 250 255  
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr  
 260 265 270  
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala  
 275 280 285  
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr  
 290 295 300  
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr  
 305 310 315  
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala  
 320 325 330  
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu  
 335 340 345  
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala  
 350 355 360  
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val  
 365 370 375  
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser  
 380 385 390  
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr  
 395 400 405  
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro  
 410 415 420  
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly  
 425 430 435  
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro  
 440 445 450  
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile  
 455 460 465  
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
 470 475 480  
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
 485 490 495  
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
 500 505 510  
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys  
 515 520 525  
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

530

535

540

Ser Pro Glu Asp

<210> 119  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 119  
 cgggacagga gacccagaaa ggg 23

<210> 120  
 <211> 24  
 <212> DNA  
 <213> Artificial

B1  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 120  
 ggccaagtga tccaaggcat cttc 24

<210> 121  
 <211> 49  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-49  
 <223> Synthetic construct.

<400> 121  
 ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122  
 <211> 1778  
 <212> DNA  
 <213> Homo sapiens

<400> 122  
 gagataggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50  
 tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
 gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
 ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
 gctcaagttt tcaactatca tctattccac cgtgttctgg ctgattgggg 300  
 ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctcct 400  
 gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
 ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550  
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600  
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
 aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
 cgactgcagt gcccctggac ccctggcctg tggggtgccc tacacctgct 750  
 gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
 atcgacaagg agcgtttcag tgtgcaggat gtcacttacg tgcggggctg 850  
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
 gcctcctcct gggcatcctg cttccccagt tctgggggt gctgctgacg 950  
 ctgctgtaca tcacccgggt ggaggacatc atcatggagc actctgtcac 1000  
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050  
 cgggatgctg cttgtgctac cccaattagg gccagcctg ccatggcagc 1100  
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
 ggacagggt gcggcccctc tgcccacact cagtactgac caaagccagg 1200  
 gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc cccagggagc 1250  
 agagcctggg cctcccctaa gaggccttcc ccgaggcagc tctggaatct 1300  
 gtgcccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350  
 ctacagggga gggagagcct gaggcctctg tcagggccca tttcatctct 1400  
 ggcagtgcct tggcgggtgg attcaaggca gttttgtagc acctgtaatt 1450  
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500  
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550  
 ctcttctcag cctcccagggt gccttgagcc ctcttgcaag ggcggctgct 1600  
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
 gtcttattct tgcccttccc ccaaccagtt tgттаatcaa acaataaaaa 1750  
 catgttttgt tttgttttta aaaaaaaa 1778

<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123

Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
 1 5 10 15  
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val  
 20 25 30  
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
 35 40 45  
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60  
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
 65 70 75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
 80 85 90  
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
 95 100 105  
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
 110 115 120  
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
 125 130 135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165  
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
 170 175 180  
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
 185 190 195  
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
 200 205 210  
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
 215 220 225  
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

B1

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens



<400> 127

B1  
gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100  
ctctgtgggt tgctggcagc caccttgatc caagccaccc tcagtccac 150  
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350  
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450  
gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500  
tggacaccag tgcaagtggc cccaccgcc tggtcctcag tgactgtgcc 550  
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct 600  
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650  
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700  
ggcatgtatg cagacctcct gcagctgggt aaggtgcca tttccctcag 750  
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800  
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850  
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900  
caacatcccg ttcagcctca tcgtgagtca ggacgtgggt aaagctgcag 950  
tggctgctgt gctctctcca gaagaattca tggtcctgtt ggactctgtg 1000  
cttcctgaga gtgccatcg gctgaagtca agcatcgggc tgatcaatga 1050  
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100  
aggacactcc cgagtttttt atagaccaag gccatgcca ggtggcccaa 1150  
ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200  
caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250  
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400  
gatctggggg ccagtggtca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500  
 gaaacccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550  
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600  
 cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

<400> 128

Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala  
 1 5 10 15  
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile  
 20 25 30  
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
 35 40 45  
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
 50 55 60  
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
 65 70 75  
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
 80 85 90  
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
 95 100 105  
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
 110 115 120  
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
 125 130 135  
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
 140 145 150  
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
 155 160 165  
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu  
 170 175 180  
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
 185 190 195  
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
 200 205 210  
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
 215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys  
 230 235 240  
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser  
 245 250 255  
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu  
 260 265 270  
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser  
 275 280 285  
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu  
 290 295 300  
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His  
 305 310 315  
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp  
 320 325 330  
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr  
 335 340 345  
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu  
 350 355 360  
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu  
 365 370 375  
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr  
 380 385 390  
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp  
 395 400 405  
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp  
 410 415 420  
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu  
 425 430 435  
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu  
 440 445 450  
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys  
 455 460 465  
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
 470 475 480

Pro Val Ser Gln

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcgggtttt ggtgtgtctc tgtgaccatg 50  
gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100  
aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150  
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400  
aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaac 450  
ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcagctgag 500  
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600  
ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650  
aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700  
atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750  
atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800  
tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850  
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900  
agcgaaagat aatgtgtgtg gctgggtattg gacttgttgt attattcttc 950  
agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000  
ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050  
ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100  
gtatattttg tattacctct ttttttcaag tgatttaaata agttaatcat 1150  
ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200  
ctgagggtatt tgaaaataat taccctctta accttctctt cccagtgaac 1250  
tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300  
aactactact ttgttttagt tagaaciaag ctcaaaacta ctttagtta 1350  
cttggctatc tgattttata ttgccttatc caaagatggg gaaagtaagt 1400  
cctgaccagg tgttcccaca tatgcctggt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcac 1500  
 tttccttttg agtagagaaa ttatgtgtgt catgtggtct tctgaaaatg 1550  
 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600  
 ctctctctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650  
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700  
 gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750  
 tccatctcct tagttttctt ttaaggtgac ccatctgtga taaaaatata 1800  
 gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850  
 aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900  
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950  
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000  
 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050  
 attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100  
 tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150  
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200  
 aaaaaaaaaa aaa 2213

<210> 130  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
 Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val  
 1 5 10 15  
 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln  
 20 25 30  
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met  
 35 40 45  
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
 50 55 60  
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile  
 65 70 75  
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys  
 80 85 90  
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg  
 95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp  
 110 115 120  
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser  
 125 130 135  
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg  
 140 145 150  
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln  
 155 160 165  
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val  
 170 175 180  
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu  
 185 190 195  
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met  
 200 205 210  
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys  
 215 220 225  
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg  
 230 235 240  
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn  
 245 250 255  
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His  
 260 265 270  
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu  
 275 280 285  
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys  
 290 295 300  
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser  
 305 310 315  
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr  
 320 325 330  
 Ser Phe Leu Met Ser  
 335

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
 aagcaaccaa actgcaagct ttgggagttg ttcgctgtcc ctgccctgct 50  
 ctgctaggga gagaacgcca gagggaggcg gctggcccgg cggcaggctc 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200  
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250  
 aggttaacat ttcattcagg aagtcaggta gtgaaacttc cttttatcaa 300  
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350  
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450  
 atggatggat gtcattggaga ggcattggcta ccgaacacag aaatttgga 500  
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550  
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600  
 taatcttatt cgtaacagga ctaaagtcag agtgatggaa agggattggc 650  
 agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700  
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750  
 ttcaccatct tctggagaaa attttgatc ttcaacattt cacacatctc 800  
 tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850  
 tcacctttgt cagaaatgca cctgtagat tattactctt cttatacaaa 900  
 aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950  
 tttattatgc tatgtgtgct gagacagatg ccattgcttg tgaaattatt 1000  
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050  
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100  
 gcatgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150  
 attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200  
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250  
 gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300  
 gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350  
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400  
 cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450  
 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500  
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600  
 ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650  
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750  
 ttctagagat acatataaat atattacaag atcataatta tgtatttttaa 1800  
 atgaaacagt ttttaataatt accaagtttt ggccgggcac agtggctcac 1850  
 acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggctc 1900  
 aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950  
 aaatacaaaa attagctggg cgcggtggtg cacacctata gtctcagcta 2000  
 ctgagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050  
 agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100  
 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150  
 tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200  
 aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250  
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300  
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350  
 taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450  
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala  
 1 5 10 15  
 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys  
 20 25 30  
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
 35 40 45  
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
 50 55 60  
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
 65 70 75



Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly  
 80 85 90  
 Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu  
 95 100 105  
 Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly  
 110 115 120  
 Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His  
 125 130 135  
 His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala  
 140 145 150  
 Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg  
 155 160 165  
 Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr  
 170 175 180  
 Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr  
 185 190 195  
 Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr  
 200 205 210  
 Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His  
 215 220 225  
 Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys  
 230 235 240  
 Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr  
 245 250 255  
 Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys  
 260 265 270  
 Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu  
 275 280 285  
 Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu  
 290 295 300  
 Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly  
 305 310 315  
 Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr  
 320 325 330  
 Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile  
 335 340 345  
 Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile  
 350 355 360  
 Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn

	365		370		375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe	Lys		
	380		385		390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu	Ser		
	395		400		405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu	Arg		
	410		415		420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser	Ile		
	425		430		435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu	Thr		
	440		445		450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp	Gln		
	455		460		465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser	Val		
	470		475		480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser	Ile		
	485		490		495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His	Gln		
	500		505		510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp	Gln		
	515		520		525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val			
	530		535		

<210> 133  
 <211> 1475  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
 gagagaagtc agcctggcag agagactctg aaatgaggga ttagaggtgt 50  
 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100  
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200  
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
 catcaccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350  
 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctctccctg 400  
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccagagcc aaagacagag tggcggttagc aggtggagtc tttttcatcc 500  
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatac 550  
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650  
 ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700  
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750  
 gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
 cagggtatgt gtgaagaacc agggggccaga gctgggggggt ggctgggtct 850  
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900  
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950  
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000  
 attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050  
 gctcccctgc cctaagtccc caaccctcaa cttgaaaccc cattccctta 1100  
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150  
 ccccaaacc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200  
 ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250  
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300  
 cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg 1350  
 actccacagt gtccagacta atttggtcat gaactgaaat aaaaccatcc 1400  
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu  
 1 5 10 15  
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp  
 20 25 30  
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

	50	55	60
Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Pro	Ala
65		70	75
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser	Ala Ile
80		85	90
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Arg	Cys Thr
95		100	105
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala	Val Ala
110		115	120
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe	Ile Pro
125		130	135
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr	Ser Pro
140		145	150
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala	Leu Tyr
155		160	165
Leu Gly Ile Ile Ser	Ser Ser Leu Phe	Ser Leu Ile Ala	Gly Ile Ile
170		175	180
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn	Tyr Tyr
185		190	195
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser	Pro Arg
200		205	210
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser	Tyr Ser
215		220	225
Leu Thr Gly Tyr Val			
230			

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaagg 100  
 aagtcacgc tcccgtggc tcagaaccat ggctgtgcca gccggcacc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcca atgtgggtccc cctgcacct 250  
 tctggccctg ctttgagctc tgctgtcttg attccttttg cctcaciaaac 300  
 gattttgttg tgaagctgaa gggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
 1 5 10 15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
 65 70 75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
 80 85 90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
 95 100 105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
 110 115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
 ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50  
 gtctttgccca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtgggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgcga ctcagcccgg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
 tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys	1	5	10	15
Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	20	25	30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	35	40	45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	50	55	60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	65	70	75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	80	85	90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	95	100	105	
Cys	Arg	Ser	Val	Ser											110			

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

gggggcgggg gcctggagca cggcgctggg gccgcccga gcgctcactc 50  
 gctcgcactc agtcgcggga ggcttccccg cgccggccgc gtcccggccg 100  
 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggctgc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
 tctcttctctg gctgcgtccc taggtccggt ggcagccttc aaggctcgcca 250  
 cgccgtattc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300  
 tgcaggctct tgggccctgt ggacaaaggg cacgatgtga ccttctacaa 350  
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400  
 ggcccatccg caacctcacg ttccaggacc ttcacctgca ccatggaggc 450  
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500  
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
 ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600  
 caccactcgg agcacagggt ccatgggtgcc atggagctgc aggtgcagac 650  
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700  
 atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750  
 ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800  
 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850  
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
 ataccgagg ccaaagtcag gcacccctg tcctatgtgg ccagcgga 950  
 gccttctgag tctggggcgc atctgcttcc ggagcccagc acccccctgt 1000  
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050  
 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150  
 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200  
 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
 atggggatgc tggacggctc agcccctggt ccaaggattt tggggtgctg 1300  
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgctc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

B1

tggggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500  
 ccccggtggcc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550  
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgcttgccca 1600  
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650  
 gatctgtcaa cagggttaagt caatctgggg cttccactgc ctgcattcca 1700  
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750  
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800  
 gttgccccac cactggaga tgggtgctgag ggaggtgggt ggggccttct 1850  
 gggaaggtga gtggagaggg gcacctgccc ccgcccctcc ccatccccta 1900  
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccacctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly  
 1 5 10 15  
 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val  
 20 25 30  
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
 35 40 45  
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
 50 55 60  
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
 65 70 75  
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
 80 85 90  
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
 95 100 105  
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
 110 115 120  
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
 125 130 135  
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu



	140		145		150
Ile Arg His His His Ser Glu His Arg	155	Val His Gly Ala Met Glu	160		165
Leu Gln Val Gln Thr Gly Lys Asp Ala	170	Pro Ser Asn Cys Val Val	175		180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu	185	Asn Ile Thr Ala Ala Ala	190		195
Leu Ala Thr Gly Ala Cys Ile Val Gly	200	Ile Leu Cys Leu Pro Leu	205		210
Ile Leu Leu Leu Val Tyr Lys Gln Arg	215	Gln Ala Ala Ser Asn Arg	220		225
Arg Ala Gln Glu Leu Val Arg Met Asp	230	Ser Asn Ile Gln Gly Ile	235		240
Glu Asn Pro Gly Phe Glu Ala Ser Pro	245	Pro Ala Gln Gly Ile Pro	250		255
Glu Ala Lys Val Arg His Pro Leu Ser	260	Tyr Val Ala Gln Arg Gln	265		270
Pro Ser Glu Ser Gly Arg His Leu Leu	275	Ser Glu Pro Ser Thr Pro	280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val	290	Phe Phe Pro Ser Leu Asp	295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu	305	Val Ile	310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 cccacgcgtc cgcgcctctc cttctgtctg gaccttcctt cgtctctcca 50  
 tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac 100  
 cttagacctc ctttctgcc ctcctttcct gccacgcgt gcttctggc 150  
 ctttctccga cccgcgtcta gcagcagacc tcctgggggc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250  
 ccgctcccg accagcgcc tgaccctggg gaaaggatgg ttcccgaggt 300  
 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650  
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700  
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800  
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900  
tgggagaaag agaggcccg gcaccccgag cccactggc ctcagcgccc 950  
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000  
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100  
tcggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150  
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200  
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250  
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400  
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500  
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550  
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
ggccagtcca gacaaagtga ccaagacata acaagacct aacagttgca 1650  
gatatgagct gtataattgt tggtattata tattaataaa taagaagttg 1700  
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
<211> 451  
<212> PRT  
<213> Homo sapiens  
<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala  
 1 5 10 15  
 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp  
 20 25 30  
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser  
 35 40 45  
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg  
 50 55 60  
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His  
 65 70 75  
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln  
 80 85 90  
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg  
 95 100 105  
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His  
 110 115 120  
 Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro  
 125 130 135  
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys  
 140 145 150  
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro  
 155 160 165  
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu  
 170 175 180  
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg  
 185 190 195  
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly  
 200 205 210  
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe  
 215 220 225  
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val  
 230 235 240  
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly  
 245 250 255  
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg  
 260 265 270  
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly  
 275 280 285  
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

	290		295		300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro	305		310		315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg	320		325		330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser	335		340		345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala	350		355		360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu	365		370		375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His	380		385		390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala	395		400		405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro	410		415		420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala	425		430		435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys	440		445		450

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
 ctagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50  
 cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100  
 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gtcctcggtt atcgtgaccc cgggagagcg gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400  
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500  
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 ttttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
 35 40 45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
 50 55 60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
 65 70 75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
 80 85 90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50  
 ttgaggggaa gaggtgact gtacgttcct tctactctgg caccactctc 100  
 caggctgcca tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacctgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450  
 tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500  
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600  
 gcaaacagag aagatctacg tgttagatgg gacacagaat gacacagcct 650  
 ttgtcttccc aaggctgctg gacttcaccc ttgccatggc tgcccggaaa 700  
 gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggg 750  
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
 aaccgaacag tgggtggacag ctcaagtatt ccagcagagg ggctgatccc 900  
 cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
 ctggccaagt tagatccaca gacctggac acagagcagc agtgggacac 1050  
 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
 tctatgtcgt ctataacacc cgtcctgcc a gtcgggccc catccagtgc 1150  
 tcctttgatg ccagcggcac cctgaccct gaacgggcag cactccctta 1200  
 ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
 catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400  
 ttctcattc ttcaaagtgt ggccagttgt ggctcaaate ctctatattt 1450  
 ttagccaatg gcaatcaaatt tctttcagct cctttgtttc atacggaact 1500  
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
 ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600  
 cccagaccca gggctetaac cttgtatgcg ggcaggcca gggagcaggc 1650  
 agcagtgttc ttcccctcag agtgacttgg ggaggagaa ataggaggag 1700  
 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750  
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

B1

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp  
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met  
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln  
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn  
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala  
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu  
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro  
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys  
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys  
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg  
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln  
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala  
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala  
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr  
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro  
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln  
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser  
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala  
 260 265 270  
 Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala  
 275 280 285  
 Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys  
 290 295 300  
 Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro  
 305 310 315  
 Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr  
 320 325 330  
 Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile  
 335 340 345  
 Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala  
 350 355 360  
 Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu  
 365 370 375  
 Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly  
 380 385 390  
 Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu  
 395 400 405

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50  
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100  
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
 gtttctgtgc tcttaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggaggggagc atctctctga ggctggaaaa cattactgtg 500



ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
 tttccatcac gggatatggt gatagagaca tccagctact ctgtcagtcc 650  
 tcgggctggg tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700  
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750  
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800  
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850  
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950  
 ttctttctca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050  
 tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg 1100  
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250  
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
 cattaaatcc ccgttttacc agcgtcttcc ccaggacccc acctacaaaa 1400  
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
 aatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500  
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550  
 atagtcactt gccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
 acattcttct ttagggatat taaggctctt ctcccagatc caaagtcccg 1750  
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800  
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850  
 cattacattt agtttgcctt cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050  
aa 2052

<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly  
1 5 10 15  
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala  
20 25 30  
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
35 40 45  
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
50 55 60  
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
65 70 75  
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
80 85 90  
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
95 100 105  
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
110 115 120  
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
125 130 135  
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
140 145 150  
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
155 160 165  
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
170 175 180  
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
185 190 195  
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
200 205 210  
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
215 220 225  
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230 235 240  
 Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys  
 245 250 255  
 Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp  
 260 265 270  
 Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys  
 275 280 285  
 His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys  
 290 295 300  
 Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro  
 305 310 315  
 Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val  
 320 325 330  
 Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val  
 335 340 345  
 Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp  
 350 355 360  
 Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His  
 365 370 375  
 Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr  
 380 385 390  
 Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr  
 395 400 405  
 Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe  
 410 415 420  
 Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg  
 425 430 435  
 Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn  
 440 445 450  
 Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu  
 455 460 465  
 Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu  
 470 475 480  
 Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu  
 485 490 495  
 Pro Arg Gly Glu Met  
 500

<210> 149

<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgctgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggcttcctt 50  
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250  
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350  
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tgggogactg ctggaccctc ttccaccacc tttcaggcgc 450  
 cgctcggccc ctcgccgacc acccctccgg cggcggaacg cacttcgacc 500  
 acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550  
 tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600  
 ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650  
 ctccccaccc cacttgccac cgaggccccc tcttcgcctc ctccagagta 700  
 tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750  
 agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800  
 gaaacctgca aagagggcct ttacctaata tacacttctg ggctctgtca 850  
 gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacagg 900  
 aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaataa 950  
 aaaaggctgc tactctcaag gaccatactg gtttaaacia aggaggatga 1000  
 gggtcataga ttacaaaaat attttatata cttttattct cttactttat 1050  
 atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100  
 tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150  
 atttcatggg aaaaaattat tgaagaataa atctgcttcc tggaagggct 1200  
 ttcaggcatg aaacctgcta ggagggttag aaatgttctt atgtttatta 1250  
 atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300  
 taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350  
 ggtaccctaa tttatttaac tagtggttag tagactggtt ttactctatt 1400  
 taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
 aactattatg ttatttgagg gtaatttaac ctagtggaat aatgtactgt 1500  
 tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550  
 tatgtgaggc acttggtttt ttgtggaccc caagtcaaaa aactgaagag 1600  
 acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650  
 tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700  
 agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750  
 taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800  
 ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atacttttagc 1900  
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950  
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
 ctcacgcctg taatcctagc actttgggag gccaaaggcgg gtggatcact 2050  
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgtct 2100  
 ctactaaaaa tacaaacaaa ttagctgggc gtggtggcac acacctgtag 2150  
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200  
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250  
 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153  
 <211> 258  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys  
 1 5 10 15  
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn  
 20 25 30  
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro  
 35 40 45  
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala  
 50 55 60  
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala  
 65 70 75  
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro  
 80 85 90  
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr  
 95 100 105  
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala  
 110 115 120  
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro  
 125 130 135  
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val  
 140 145 150  
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro  
 155 160 165  
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

	170	175	180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys	Asn
	185	190	195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln	Thr
	200	205	210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His	Cys
	215	220	225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly	Leu
	230	235	240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile	Pro
	245	250	255
Cys Asn Arg			

B1

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 154  
 aactgctctg tggttggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgagcag ttagacctg ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggcttt ggtctcggtg cccagggccc aggcctgtgt gttgggaaga 100  
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150  
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200  
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcca tcatcttcac tcagctggag 400  
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600  
 gggctcctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90



Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

B1

<400> 159  
 aacagacggt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50  
 gctgctgctg ccctgctct gggggaggga gagggcggaa ggacagacaa 100  
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150  
 gtccatgtgc cctgctcctt ctectacccc tcgcatggct ggatttacct 200  
 tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250  
 aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300  
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
 gtatggagaa aggaagtata aatggaatt ataaacatca ccggctctct 450  
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
 gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600  
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650  
 gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
 tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900  
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
 gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100  
 tggagccaca gccctgggtct tcctgtcctt ctgcgtcatc ttcgttgtag 1150  
 tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcagggggc 1250  
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300  
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttccaga tgggtgaagcc ttgggactcg cggggacagg aggccactga 1400  
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450  
 accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550  
 atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600  
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160  
 <211> 463  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala  
 1 5 10 15  
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr  
 20 25 30  
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr  
 35 40 45  
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr  
 50 55 60  
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala  
 65 70 75  
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg  
 80 85 90  
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser  
 95 100 105  
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110 115 120

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu  
125 130 135

Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile  
140 145 150

Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser  
155 160 165

Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp  
170 175 180

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser  
185 190 195

Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser  
200 205 210

Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn  
215 220 225

Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr  
230 235 240

Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly  
245 250 255

Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu  
260 265 270

Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu  
275 280 285

Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser  
290 295 300

Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala  
305 310 315

Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln  
320 325 330

Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val  
335 340 345

Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe  
350 355 360

Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys  
365 370 375

Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu  
380 385 390

Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr  
395 400 405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

B1

<400> 161  
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgcctttcac 100  
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200  
 aaggtgacag ccctgggcg tgggaagttg gaagccacgt tcacattcat 250  
 gagggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400  
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500  
 tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccga 550  
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcctt 650  
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
 1 5 10 15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

	20		25		30									
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
			35						40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50						55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65						70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80						85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95						100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110						115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125						130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140						145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155						160					165
Cys	Val	Pro	Glu	His										
			170											

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.

<400> 165  
gtcctccgga aagtccttat c 21

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial

B1 <220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 166  
gcctagtgtt cgggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 167  
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 168  
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50  
 cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150  
 gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200  
 ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtgggg 250  
 cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300  
 ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350  
 ctgtgagcag acccggacag cactgagtc cttccccac ccggcttca 400  
 acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
 atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500  
 ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600  
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650  
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
 gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
 attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800  
 ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850  
 acaattagac tggaccacc caccacagcc catcaccctc catttccact 900  
 tgggtgttgg ttctgttca ctctgttaat aagaaaccct aagccaagac 950  
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000  
 taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050  
 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100  
 tgtatcccca gccccaaga cagctcctgg ccatatatca aggtttcaat 1150  
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaa 1204

<210> 170  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
 1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro  
                             20                            25                            30  
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu  
                             35                            40                            45  
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala  
                             50                            55                            60  
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His  
                             65                            70                            75  
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr  
                             80                            85                            90  
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys  
                             95                            100                            105  
 Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val  
                             110                            115                            120  
 Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys  
                             125                            130                            135  
 Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr  
                             140                            145                            150  
 Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn  
                             155                            160                            165  
 Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly  
                             170                            175                            180  
 Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly  
                             185                            190                            195  
 Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn  
                             200                            205                            210  
 Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala  
                             215                            220                            225  
 Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val  
                             230                            235                            240  
 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn  
                             245                            250

<210> 171  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.



<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggcttcc gggtg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
 tgtgaccaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
 atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750  
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850  
 ttgcaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
 aaaaaaa 907

<210> 180  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe	1	5	10	15
Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	20	25	30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150	

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 181  
 gtgtttctgct ggagccgatg cc 22

<210> 182  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 182  
 gacatggaca atgacagg 18

<210> 183  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 183  
 ccttttcagga tgtaggag 18

<210> 184  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 184  
gatgtctgcc accccaag 18

<210> 185  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-27  
<223> Synthetic construct.

<400> 185  
gcatcctgat atgacttgct acgtggc 27

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 186  
tacaagaggg aagaggagtt gcac 24

<210> 187  
<211> 52  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-52  
<223> Synthetic construct.

<400> 187  
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
cc 52

<210> 188  
<211> 573  
<212> DNA  
<213> Homo sapiens

<400> 188  
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50  
ctctttggag ctgtgactca gaaaacaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aacctggat 150  
 atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt. 200  
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250  
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
 atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350  
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550  
 ccaaataaag tacttatatt ctc 573

<210> 189  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 189  
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser  
 1 5 10 15  
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
 20 25 30  
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
 35 40 45  
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
 50 55 60  
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
 65 70

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 190  
 agggaccatt gcttcttcca ggcc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450  
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500  
gccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700  
atgcctgcca ggggtgattct gggggcccc tgggtgtgtgg gggagtcctt 750  
caaggctctg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000  
 gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050  
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194

Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser  
 1 5 10 15  
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg  
 20 25 30  
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu  
 35 40 45  
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala  
 50 55 60  
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His  
 65 70 75  
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly  
 80 85 90  
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His  
 95 100 105  
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val  
 110 115 120  
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr  
 125 130 135  
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His  
 140 145 150  
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser  
 155 160 165  
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile  
 170 175 180  
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala  
 185 190 195  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu



	200		205		210
Gln Gly Leu Val	Ser Trp Gly Ser Val	Gly Pro Cys Gly Gln Asp			
	215	220		225	
Gly Ile Pro Gly Val	Tyr Thr Tyr Ile	Cys Lys Tyr Val Asp Trp			
	230	235		240	
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50  
 ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100  
 tcgcatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150  
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350  
 caagaccac ctggagatga agaagatgat ctgagaggtg acaggagggg 400  
 tcagtacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450  
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500  
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550  
 tgccctgagg accccgcctg gactccccag ctttcccacc ccatacctcc 600  
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650  
 tttgtttggt cattgagggt ttgtttgtgt tttcatcaat gtctttgtaa 700  
 agcaciaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750  
 ttgggtcccc tcctctctt cttccctcct tccccgctcc ctgtgcagaa 800  
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850  
 cttccagcct gtgttcccct cacttgaggg aaccagcact ctccatcctt 900  
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950  
 gaccccaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000  
 cctctttcgg gtttccttgg acagtgccat gggtccagtg ctctggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
 attccacacc tcttctcatc ctcaagtgatg tgaaggtggg aaggaaagga 1150  
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200  
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250  
 tactgtccct tactggggca gcagagggtc tcggaggcag aagtgaggcc 1300  
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350  
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
 aagtçagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450  
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 196  
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe  
 1 5 10 15  
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn  
 20 25 30  
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu  
 35 40 45  
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
 50 55 60  
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met  
 65 70 75  
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys  
 80 85 90  
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr  
 95 100 105  
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu  
 110 115 120  
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro  
 125 130 135  
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro  
 140 145 150

<210> 197  
 <211> 4842  
 <212> DNA  
 <213> Homo sapiens

<400> 197

B1  
cgcgctcccc gcgcgcctcc tcgggctcca cgcgtcttgc cccgcagagg 50  
cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100  
ggggtcggcg ccgccgtgcg cgcccgcttg gcgctggcct tggcgctggc 150  
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200  
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250  
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300  
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350  
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400  
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450  
ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500  
tgagtgaaaa ccagatccag gggatcccga ggaaggcgtt ccgcggcatc 550  
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600  
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650  
acaacaacat cagtcgcata ctggtcacca gcttcaacca catgccgaag 700  
atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750  
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cagaagaagg agtacgtgtg cccagcccc cactcggagc cccatcctg 900  
caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950  
tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000  
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050  
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agaatcagat atcggatatt gctccagatg ccttccaggg cctgaaatca 1150  
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atcgagacaa gcggggcccg ctgcagcagc ccgcgccgac tcgccaacaa 1500  
 gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550  
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 ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtggc 1900  
 ctcaaaacct tgatgctgag gagtaacttg atcagctgtg tgagtaatga 1950  
 cacctttgcc ggctgagtt cggtgagact gctgtccctc tatgacaatc 2000  
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 gctcggcaag tggttgagga agaggcggat cgtcagtggg aaccctaggt 2150  
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 caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250  
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 agcccacctg ccgtgccca ccaggcttcg ccggccccag atgcgagaag 3550  
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gcccacatg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550  
cccgcagcaa gcggcggaac tacgtcttcc agtgcacgga cggctcctcg 4600  
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ctaagcccct gcccgcctgc ctgccacctc tcggactcca gcttgatgga 4700  
gttgggacag ccatgtggga ccccctggtg attcagcatg aaggaaatga 4750  
agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800  
aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198  
<211> 1523  
<212> PRT  
<213> Homo sapiens

<400> 198  
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg  
1 5 10 15  
Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro  
20 25 30  
Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val  
35 40 45  
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro  
50 55 60  
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg  
65 70 75  
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu  
80 85 90  
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe  
95 100 105  
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys  
110 115 120  
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu  
125 130 135  
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg  
140 145 150  
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp  
155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu  
 170 175 180  
 Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg  
 185 190 195  
 Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu  
 200 205 210  
 Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp  
 215 220 225  
 Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr  
 230 235 240  
 Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp  
 245 250 255  
 Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro  
 260 265 270  
 Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr  
 275 280 285  
 Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu  
 290 295 300  
 Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu  
 305 310 315  
 Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr  
 320 325 330  
 Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp  
 335 340 345  
 Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu  
 350 355 360  
 Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe  
 365 370 375  
 Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys  
 380 385 390  
 Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu  
 395 400 405  
 Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys  
 410 415 420  
 Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala  
 425 430 435  
 Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp  
 440 445 450  
 Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser

455 460 465  
 Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser  
 470 475 480  
 Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe  
 485 490 495  
 Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg  
 500 505 510  
 Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg  
 515 520 525  
 Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn  
 530 535 540  
 Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys  
 545 550 555  
 Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys  
 560 565 570  
 Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu  
 575 580 585  
 Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val  
 590 595 600  
 Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn  
 605 610 615  
 Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser  
 620 625 630  
 Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr  
 635 640 645  
 Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu  
 650 655 660  
 Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly  
 665 670 675  
 Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys  
 680 685 690  
 Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala  
 695 700 705  
 Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln  
 710 715 720  
 Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val  
 725 730 735  
 Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met  
 740 745 750



Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr  
 755 760 765  
 Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile  
 770 775 780  
 Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe  
 785 790 795  
 Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg  
 800 805 810  
 Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu  
 815 820 825  
 Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu  
 830 835 840  
 Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly  
 845 850 855  
 Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu  
 860 865 870  
 Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser  
 875 880 885  
 Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr  
 890 895 900  
 His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala  
 905 910 915  
 Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr  
 920 925 930  
 Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr  
 935 940 945  
 Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile  
 950 955 960  
 Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser  
 965 970 975  
 His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly  
 980 985 990  
 Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys  
 995 1000 1005  
 Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys  
 1010 1015 1020  
 Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile  
 1025 1030 1035  
 Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

1040 1045 1050  
 Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly  
 1055 1060 1065  
 Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala  
 1070 1075 1080  
 His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly  
 1085 1090 1095  
 Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu  
 1100 1105 1110  
 His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln  
 1115 1120 1125  
 Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu  
 1130 1135 1140  
 Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu  
 1145 1150 1155  
 Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu  
 1160 1165 1170  
 Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln  
 1175 1180 1185  
 Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp  
 1190 1195 1200  
 Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu  
 1205 1210 1215  
 Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val  
 1220 1225 1230  
 Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr  
 1235 1240 1245  
 Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys  
 1250 1255 1260  
 Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser  
 1265 1270 1275  
 Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala  
 1280 1285 1290  
 Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys  
 1295 1300 1305  
 Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala  
 1310 1315 1320  
 Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys  
 1325 1330 1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
 1340 1345 1350  
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
 1355 1360 1365  
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
 1370 1375 1380  
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
 1385 1390 1395  
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
 1400 1405 1410  
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
 1415 1420 1425  
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
 1430 1435 1440  
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
 1445 1450 1455  
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
 1460 1465 1470  
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
 1475 1480 1485  
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
 1490 1495 1500  
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
 1505 1510 1515  
 Glu Cys Gly Cys Leu Ala Cys Ser  
 1520

<210> 199  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 199  
 atggagattc ctgccaaactt gccg 24

<210> 200  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

B1  
<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcatcg tcgaaatag cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct tttagttct gtctccggca ggctttgagg atgaaggctg 150  
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600  
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccgt ttctcccaa tattccttct caaacttggg 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaa 750  
gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203

Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
 1 5 10 15  
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
 20 25 30  
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
 35 40 45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
 50 55 60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
 65 70 75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
 80 85 90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
 95 100 105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
 110 115 120  
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
 125 130 135  
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
 140 145

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
ctcattggct gcctggtcac aggc 24

<210> 206  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 206  
ccagtcggac aggtctctcc cctc 24

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 207  
tcagtgacca aggctgagca ggcg 24

<210> 208  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 208  
ctacactcgt tgcaaactgg caaaaatatt ctcgaggggt ggcctgg 47

<210> 209  
<211> 1648  
<212> DNA  
<213> Homo sapiens

<400> 209  
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50  
cctcagcagt gtcattgtgt aaaaacgcc aactgaatat atcatgcccc 100  
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
 gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcagttggt 450  
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550  
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagagggtt 600  
 catctgatcg tggcagggtg ttatgacgag agagtcctgg agaattgtga 650  
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
 atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750  
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
 tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850  
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
 gagcctgacc cggtgcactt ctcagaagca atagaaaagt tcatccgtga 950  
 accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000  
 aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050  
 aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100  
 ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150  
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaatgtgg 1300  
 tgtcattcca tgttcagcag agtattttaa ttatattttc tcgggattat 1350  
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450  
 ataagagag cagggtatt gtagttccca gattcaatcc accgaagtgt 1500  
 tcactgtcat ctgttaggga atttttgttt gtccctgtctt tgccctggatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210  
 <211> 323

<212> PRT  
 <213> Homo sapiens

<400> 210

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly  
 1 5 10 15  
 Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val  
 20 25 30  
 Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His  
 35 40 45  
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg  
 50 55 60  
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly  
 65 70 75  
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val  
 80 85 90  
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val  
 95 100 105  
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro  
 110 115 120  
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu  
 125 130 135  
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala  
 140 145 150  
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp  
 155 160 165  
 Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg  
 170 175 180  
 Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val  
 185 190 195  
 Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe  
 200 205 210  
 Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val  
 215 220 225  
 Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu  
 230 235 240  
 Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly  
 245 250 255  
 Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu  
 260 265 270



Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211  
 <211> 1554  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50  
 cttcgcgatc ttccgcgtta ctttcttgct ggcgttggtg ggagccgtgc 100  
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200  
 tttgcatgag ttcctgggta atttgcata gagatatggg cctgtggtct 250  
 ccttctgggt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300  
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400  
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctggt acacagatgg taatgggttag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggcttcc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
 tgggtacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200  
 gatcgggttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250  
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300  
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212  
 <211> 462  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
 1 5 10 15  
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala  
 20 25 30  
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu  
 35 40 45  
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn  
 50 55 60  
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg  
 65 70 75  
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His  
 80 85 90  
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys  
 95 100 105  
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn  
 110 115 120  
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu  
 125 130 135  
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

140 145 150  
 Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser  
 155 160 165  
 Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val  
 170 175 180  
 Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln  
 185 190 195  
 Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu  
 200 205 210  
 Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu  
 215 220 225  
 Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys  
 230 235 240  
 Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser  
 245 250 255  
 Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser  
 260 265 270  
 Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys  
 275 280 285  
 Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys  
 290 295 300  
 Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val  
 305 310 315  
 Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu  
 320 325 330  
 Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln  
 335 340 345  
 Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg  
 350 355 360  
 Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro  
 365 370 375  
 Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp  
 380 385 390  
 Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly  
 395 400 405  
 Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr  
 410 415 420  
 Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val  
 425 430 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
 455 460

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50  
 tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100  
 tcagggcttg tgccctctcg ctctctgacg ctcttgccgc atctgggtgt 150  
 cgatcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
 gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtgcg ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450  
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600  
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tgttttgtag taacattaag acttatatac agtttttaggg gacaattaaa 750  
 aaaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
 1 5 10 15  
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
 20 25 30  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
 35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
 50 55 60  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
 65 70 75  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
 80 85 90  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
 95 100 105  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
 110 115 120  
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
 125 130 135  
 Lys Lys Lys Pro Phe  
 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccggaccc tgccgcctg ccactatgtc ccgccgtct atgctgcttg 50  
 cctgggctct cccagcctc ctgcgactcg gagcggtca ggagacagaa 100  
 gacccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150  
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
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 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450  
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 acactctctc caggcaacca gctctaccac ctcattccaga attggccaca 600  
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<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu  
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Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys  
20 25 30  
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu  
35 40 45  
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser  
50 55 60  
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln  
65 70 75  
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp  
80 85 90  
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val  
95 100 105  
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His  
110 115 120  
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr  
125 130 135  
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly  
140 145 150  
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr  
155 160 165  
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly  
170 175 180  
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser  
185 190 195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtcctcccgg ctcagaggac 150  
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<210> 218  
<211> 252  
<212> PRT  
<213> Homo sapiens

<400> 218

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35 40 45  
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met  
50 55 60  
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala  
65 70 75  
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro  
80 85 90  
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe  
95 100 105  
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly  
110 115 120  
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln  
125 130 135  
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro  
140 145 150  
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile  
155 160 165  
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu  
170 175 180  
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro  
185 190 195  
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp  
200 205 210



Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
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Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
 245 250

<210> 219  
 <211> 2065  
 <212> DNA  
 <213> Homo sapiens

<400> 219  
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 agcgccagcc ggctgcggct gccacacagg ctcacatgg gctccgggcg 350  
 ccgggcgctg tccgcgggtgc cggccgtgct gctggtcctc acgctgccgg 400  
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
 aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaggggctc 500  
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tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
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 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650  
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 ttcaaataat ccataatctaa atttagtgca atatcttgct ttttgtatag 2000  
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 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
				20				25						30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35				40						45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55						60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala  
                                 65                                70                                75  
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr  
                                 80                                85                                90  
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe  
                                 95                                100                                105  
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr  
                                 110                                115                                120  
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile  
                                 125                                130                                135  
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe  
                                 140                                145                                150  
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val  
                                 155                                160                                165  
 Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
                                 170                                175                                180  
 Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
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 Phe Leu Val Phe Pro Leu  
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<210> 221  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 221  
 acggctcacc atgggctccg 20

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 222  
 aggaagagga gcccttggag tccg 24

<210> 223  
 <211> 40

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 223  
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

B1  
<400> 224  
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tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200  
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<210> 225  
<211> 257  
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly  
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Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu  
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Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser  
35 40 45  
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile  
50 55 60  
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly  
65 70 75  
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr  
80 85 90  
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn  
95 100 105  
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser  
110 115 120  
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn  
125 130 135  
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly  
140 145 150  
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val  
155 160 165  
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly  
170 175 180  
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr  
185 190 195  
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly  
200 205 210  
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr  
215 220 225  
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu  
230 235 240  
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg  
245 250 255

Ser Arg

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226

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 cggggcctct gctttgggga tgggaatgtg tttttctccc aaacttgttt 3800  
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30



Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser  
 35 40 45  
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn  
 50 55 60  
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln  
 65 70 75  
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val  
 80 85 90  
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg  
 95 100 105  
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro  
 110 115 120  
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser  
 125 130 135  
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg  
 140 145 150  
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn  
 155 160 165  
 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu  
 170 175 180  
 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe  
 185 190 195  
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr  
 200 205 210  
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met  
 215 220 225  
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser  
 230 235 240  
 Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala  
 245 250 255  
 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro  
 260 265 270  
 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser  
 275 280 285  
 Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys  
 290 295 300  
 Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala  
 305 310 315  
 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

320 325 330  
 Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala  
 335 340 345  
 Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly  
 350 355 360  
 Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser  
 365 370 375  
 Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe  
 380 385 390  
 Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val  
 395 400 405  
 Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys  
 410 415 420  
 Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala  
 425 430 435  
 Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe  
 440 445 450  
 Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val  
 455 460 465  
 Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn  
 470 475 480  
 Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly  
 485 490 495  
 Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile  
 500 505 510  
 Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile  
 515 520 525  
 Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu  
 530 535 540  
 Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr  
 545 550 555  
 Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys  
 560 565 570  
 Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met  
 575 580 585  
 Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro  
 590 595 600  
 Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile  
 605 610 615

B1

Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn  
 620 625 630  
 Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr  
 635 640 645  
 Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu  
 650 655 660  
 Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp  
 665 670 675  
 Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val  
 680 685 690  
 Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr  
 695 700 705  
 Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala  
 710 715 720  
 Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile  
 725 730 735  
 Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu  
 740 745 750  
 Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe  
 755 760 765  
 Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser  
 770 775 780  
 Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp  
 785 790 795  
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser  
 800 805 810  
 Phe Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln  
 815 820 825  
 Arg Asp Lys Ile Tyr Val Phe  
 830

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 <211> 2848  
 <212> DNA  
 <213> Homo sapiens

<400> 228  
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 ttgggcgctg gagggcctgt cctgaccatg gtcctgcct ggctgtggct 150  
 gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc tttataacctg 250  
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300  
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350  
 ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag 400  
 taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg 450  
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500  
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550  
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 gctgttggtg caggtcaagg acatgggtga ccaggcctca ggccaccagg 800  
 ccaactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850  
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 tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100  
 tggatgatga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150  
 acagtcagca tccctgagct cagtccacca ggtactgaag tgactagact 1200  
 gtcagcagag gatgcagatg cccccggctc cccaattcc cacgttgtgt 1250  
 atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300  
 caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccactccg 1350  
 agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400  
 cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450  
 atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500  
 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550  
 ttgatgctga cctcgagccc gccttccgcc tcatggattt tgccattgag 1600  
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 gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccca 1850  
 tcagtgtccc agccggctct ttcctgctga ccatccagcc ctccgacccc 1900  
 atcagccgaa ccctcagggt ctccctagtc aatgactcag agggctggct 1950  
 ctgcattgag aaattctccg gggaggtgca caccgcccag tccctgcagg 2000  
 gcgcccagcc tggggacacc tacacggtgc ttgtggaggc ccaggataca 2050  
 gccctgactc ttgcccctgt gccctcccaa tacctctgca caccgcca 2100  
 agaccatggc ttgatcgtga gtggaccag caaggacccc gatctggcca 2150  
 gtgggcacgg tccctacagc ttcacccttg gtcccaaccc cacggtgcaa 2200  
 cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt 2250  
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 ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848

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 <211> 807  
 <212> PRT  
 <213> Homo sapiens

<400> 229  
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 35 40 45  
 Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp  
 50 55 60  
 Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser  
 65 70 75  
 Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala  
 80 85 90  
 Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val  
 95 100 105  
 Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn  
 110 115 120  
 Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu  
 125 130 135  
 Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala  
 140 145 150  
 Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe  
 155 160 165  
 His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe  
 170 175 180  
 Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly  
 185 190 195  
 Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu  
 200 205 210  
 Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala  
 215 220 225  
 Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser  
 230 235 240  
 Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro  
 245 250 255  
 His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr  
 260 265 270  
 His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu  
 275 280 285  
 Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala  
 290 295 300  
 Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp  
 305 310 315

Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn  
 320 325 330  
 Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile  
 335 340 345  
 Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala  
 350 355 360  
 Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr  
 365 370 375  
 Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala  
 380 385 390  
 Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu  
 395 400 405  
 Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met  
 410 415 420  
 Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val  
 425 430 435  
 Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile  
 440 445 450  
 Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro  
 455 460 465  
 Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu  
 470 475 480  
 Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr  
 485 490 495  
 Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val  
 500 505 510  
 Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser  
 515 520 525  
 His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly  
 530 535 540  
 Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val  
 545 550 555  
 Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu  
 560 565 570  
 Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr  
 575 580 585  
 Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu  
 590 595 600  
 Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly

605 610 615  
 Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp  
 620 625 630  
 Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu  
 635 640 645  
 Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His  
 650 655 660  
 Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser  
 665 670 675  
 Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val  
 680 685 690  
 Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr  
 695 700 705  
 Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile  
 710 715 720  
 Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val  
 725 730 735  
 Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg  
 740 745 750  
 Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val  
 755 760 765  
 Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile  
 770 775 780  
 Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp  
 785 790 795  
 Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val  
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<210> 230  
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 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

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 cgccttaccg cgcagcccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<221> Artificial Sequence  
<222> full  
<223> Synthetic oligonucleotide probe

<400> 231  
cctgagctgt aaccccactc cagg 24

<210> 232  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 232  
agagtctgtc ccagctatct tgt 23

<210> 233  
<211> 2786  
<212> DNA  
<213> Homo sapiens

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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttcctgag 250  
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tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350  
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400  
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450  
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
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ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650  
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gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800  
ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggaccca 850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900  
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 atgtatccat atgggtactc agtcaaaaag gccccagatg ccgaggaact 1000  
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 agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150  
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 cctcctcttt gccttttgaa ctcaacttcaa agatctaggc ctcatcttac 2400  
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 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700  
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<210> 234  
 <211> 421  
 <212> PRT  
 <213> Homo sapiens

<400> 234

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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile  
 170 175 180  
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala  
 185 190 195  
 Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser  
 200 205 210  
 Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro  
 215 220 225  
 Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys  
 230 235 240  
 Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro  
 245 250 255  
 Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp  
 260 265 270  
 Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu  
 275 280 285  
 Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn  
 290 295 300  
 Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met  
 305 310 315  
 Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu  
 320 325 330  
 Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val  
 335 340 345  
 Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr  
 350 355 360  
 Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile  
 365 370 375  
 Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly  
 380 385 390  
 Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr  
 395 400 405  
 Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu  
 410 415 420

Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50  
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ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
cccgcccttc ctccacaaag agcacccttg cctcacaggt gtattccctc 200  
aacaccgact ttgccttccg cctataccgc aggettggtt tggagacccc 250  
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300  
tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350  
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400  
ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgacctga 450  
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tttctccaac ccctccattg cccaggcgag gatcaacagc catgtgaaaa 600  
agaagacca aggaagggtt gtagacataa tccaaggcct tgaccttctg 650  
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gccctttcac cttgaatata caagaaagaa cttcccatc ctggtgggcg 750  
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gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900  
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gtttctaaag caaccacaa ggctgtgctg gatgtcagt aagagggcac 1150  
tgaggccaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200  
gtccctctta cttcactgtc tccttcaata ggaccttct gatgatgatt 1250  
acaataaag ccacagacgg tattctcttt ctagggaaag tggaaaatcc 1300  
cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350  
tgcacaagaa ataacaaacc acatccctct ttctgttctg agggatgcatt 1400  
tgaccccagt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

aatcaccaaa ccatacaacag ggaccccagt cacaagccaa cacccattaa 1500  
 cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcatg 1550  
 ggatgttgct gggttacat atttccattc cttggggctc ccaggaatgg 1600  
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac 1650  
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236

Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys  
 1 5 10 15  
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr  
 20 25 30  
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
 35 40 45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
 50 55 60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
 65 70 75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
 80 85 90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
 95 100 105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
 110 115 120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
 125 130 135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
 140 145 150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
 155 160 165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
 170 175 180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
 185 190 195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

	200		205		210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe		
	215		220		225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met		
	230		235		240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn		
	245		250		255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe		
	260		265		270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala		
	275		280		285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys		
	290		295		300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser		
	305		310		315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala		
	320		325		330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser		
	335		340		345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser		
	350		355		360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile		
	365		370		375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn		
	380		385		390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile		
	395		400		405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser			
	410		415		

<210> 237  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 237  
 caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.  
  
<400> 238  
ctttgctggtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

B1  
<400> 239  
tgactcgggg tctccaaaac cagc 24

<210> 240  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 240  
ggtataggcg gaaggcaaag tcgg 24

<210> 241  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 241  
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242  
<211> 2436  
<212> DNA  
<213> Homo sapiens

<400> 242  
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50



agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100  
 gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150  
 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200  
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250  
 aaaggaaatg ttctccttat gtttggctta ctattgcatt tagaagctgc 300  
 aacaaattcc aatgagacta gcacctctgc caaactgga tccagtgtga 350  
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400  
 agtggggcca gcacagccac catctcaggg tccagcgtga cctccaatgg 450  
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500  
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 gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600  
 caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650  
 ctgggtccag tgtgacctcc agtggagcca gcactgccac caactctgag 700  
 tccagcacag tgtccagttag ggccagcact gccaccaact ctgagtctag 750  
 cacactctcc agtggggcca gcacagccac caactctgac tccagcaca 800  
 cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850  
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 ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950  
 gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000  
 gccaccaact ctgagtccag cagacctcc agtggggcca gcacagccac 1050  
 caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100  
 ctgagtccag cagacctcc agtggggcca gcacagccac caactctgag 1150  
 tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200  
 cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250  
 tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300  
 agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350  
 ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400  
 gcactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450  
 gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500

caactctgac tccagcacia cctccagtga ggccagcaca gccaccaact 1550  
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 cgtgggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850  
 tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaacat 1900  
 ggccttggtc caggccctgg agggaaatcat ggagcccccc acaggcccag 1950  
 gtggagtcct aactgggttct ggaggagacc agtatcatcg atagccatgg 2000  
 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050  
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 cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150  
 tgaagaaggt attcctcacc tttcttgcct ttaccagaca ctggaaagag 2200  
 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250  
 acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300  
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350  
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243  
 <211> 596  
 <212> PRT  
 <213> Homo sapiens

<400> 243  
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu  
 1 5 10 15  
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser  
 20 25 30  
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala  
 35 40 45  
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala  
 50 55 60  
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val  
 65 70 75

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala  
 80 85 90  
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala  
 95 100 105  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 110 115 120  
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val  
 125 130 135  
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala  
 140 145 150  
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala  
 155 160 165  
 Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala  
 170 175 180  
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 185 190 195  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 200 205 210  
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala  
 215 220 225  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 230 235 240  
 Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala  
 245 250 255  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 260 265 270  
 Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala  
 275 280 285  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 290 295 300  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 305 310 315  
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala  
 320 325 330  
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val  
 335 340 345  
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala  
 350 355 360  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

365 370 375  
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala  
 380 385 390  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala  
 395 400 405  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
 410 415 420  
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala  
 425 430 435  
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val  
 440 445 450  
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala  
 455 460 465  
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala  
 470 475 480  
 Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala  
 485 490 495  
 Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile  
 500 505 510  
 Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe  
 515 520 525  
 Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn  
 530 535 540  
 Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly  
 545 550 555  
 Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro  
 560 565 570  
 Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile  
 575 580 585  
 Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro  
 590 595

<210> 244  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150

ccccattgag aagggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tgggggtcaac aacgtgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550

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tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
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acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
gttgtcacat cagctgacat gacctggagg gggtgggggt gggggacagg 900  
tttctgaaat ccctgaaggg gggtgtactg ggatttgtga ataaacttga 950  
tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu  
1 5 10 15  
Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu  
20 25 30  
Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg  
35 40 45  
Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His  
50 55 60  
Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met  
65 70 75  
Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu  
80 85 90  
Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile  
95 100 105  
Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn  
110 115 120  
Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln  
125 130 135  
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys  
140 145 150  
Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu  
155 160 165  
Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala  
170 175 180

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 250  
 aagcttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 251  
 tgacccatt gagaaggatca ttgaaggat caaccgagg ctg 43

<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens

<400> 252

B1  
ctccgggtcc ccaggggctg cgccggggccg gcctggcaag ggggacgagt 50  
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tgaccctgac tcaactccagg tccggaggcg gggggccccg gggcgactcg 150  
ggggcggaacc gcgggggcgga gctgccgccc gtgagtcgag ccgagccacc 200  
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250  
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300  
cctcgggcac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350  
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agcttcaagg gcaaggaccc acagcgcgac tgtcaaaact acatcaagat 650  
cctcctgccg ctcagcggca gtcacctgtt cacctgtggc acagcagcct 700  
tcagccccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750  
gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800  
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gggcgatgag ggtggagagc ggggtgctaca gcagcgctgg acctccttcc 1150  
tcaaggccca gctgctgtgc tcacggcccc acgatggctt ccccttcaac 1200  
gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250  
cacccttttc tatggggtct tcaacttcca gtggcacagg ggaactacag 1300  
aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350  
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gaccaccccg gtgcccacac cccggcctgg agcgtgcac accaacagt 1450



cccgggaaag gaagatcaac tcatccctgc agtcccaga ccgcgtgctg 1500  
 aacttcctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550  
 gctgctgctg cagccccagg ctcgctacca gcgcgtggct gtacaccgcg 1600  
 tccctggcct gcaccacacc tacgatgtcc tcttcctggg cactggtgac 1650  
 ggccggctcc acaaggcagt gagcgtgggc ccccggtgc acatcattga 1700  
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 35 40 45  
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu  
 50 55 60  
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu  
 65 70 75  
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80 85 90  
 Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr  
 95 100 105  
 Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys  
 110 115 120  
 Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile  
 125 130 135  
 Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly  
 140 145 150  
 Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn  
 155 160 165  
 Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp  
 170 175 180  
 Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala  
 185 190 195  
 Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe  
 200 205 210  
 Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro  
 215 220 225  
 Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe  
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 Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly  
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 Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu  
 260 265 270  
 Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile  
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 Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp  
 290 295 300  
 Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp  
 305 310 315  
 Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro  
 320 325 330  
 Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr  
 335 340 345  
 Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val  
 350 355 360  
 Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys  
 365 370 375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro  
 380 385 390  
 Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg  
 395 400 405  
 Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu  
 410 415 420  
 Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser  
 425 430 435  
 Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala  
 440 445 450  
 Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe  
 455 460 465  
 Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly  
 470 475 480  
 Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly  
 485 490 495  
 Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu  
 500 505 510  
 Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn  
 515 520 525  
 Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp  
 530 535 540  
 Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu  
 545 550 555  
 Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu  
 560 565 570  
 Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser  
 575 580 585  
 Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln  
 590 595 600  
 Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser  
 605 610 615  
 Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn  
 620 625 630  
 Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu  
 635 640 645  
 Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu  
 650 655 660  
 Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val

665 670 675  
 Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro  
 680 685 690  
 Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys  
 695 700 705  
 Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val  
 710 715 720  
 Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe  
 725 730 735  
 Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln  
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 Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu  
 755 760 765  
 Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr  
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 Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro  
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 Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile  
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 <213> Artificial

<220>  
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 <222> 1-24  
 <223> Synthetic construct.

<400> 254  
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<220>  
 <221> Artificial Sequence  
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<400> 255  
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<220>  
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<210> 259  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
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<223> unknown base

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<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro  
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly  
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser  
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly  
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala  
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe  
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro  
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe  
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu  
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg  
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe  
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu  
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val  
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly  
230 235 240

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val  
 245 250 255  
 Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser  
 260 265 270  
 Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys  
 275 280 285  
 Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala  
 290 295 300  
 Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu  
 305 310 315  
 His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg  
 320 325 330  
 Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser  
 335 340 345  
 Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro  
 350 355 360  
 Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu  
 365 370 375  
 Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly  
 380 385 390  
 Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu  
 395 400 405  
 Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala  
 410 415 420  
 Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly  
 425 430 435  
 Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp  
 440 445 450  
 Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val  
 455 460 465  
 Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile  
 470 475 480  
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys  
 485 490 495  
 Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser  
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 Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu  
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 His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu

530 535 540  
 Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu  
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 Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu  
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 Leu Phe Asn Ser Asp Ser Asn Pro Asp Lys Ala Lys Gln Val Glu  
 575 580 585  
 Leu Met Arg Asp Tyr Arg Ile Lys Tyr Pro Lys Ala Asp Met Gln  
 590 595 600  
 Ile Leu Pro Val Ser Gly Glu Phe Ser Arg Ala Leu Ala Leu Glu  
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 Val Gly Ser Ser Gln Phe Asn Asn Glu Ser Leu Leu Phe Phe Cys  
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 Asp Val Asp Leu Val Phe Thr Thr Glu Phe Leu Gln Arg Cys Arg  
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 Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe Pro Ile Ile Phe  
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 Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys Val Pro Ser  
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 Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp Arg Asn  
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 Arg Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe  
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 Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly  
 755 760 765  
 Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met  
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<213> Artificial

<220>  
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<223> Synthetic construct.

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<220>  
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<223> Synthetic construct.

<400> 262  
tcccatttct tccgtggtgc ccag 24

<210> 263  
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<212> DNA  
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<220>  
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<222> 1-46  
<223> Synthetic construct.

<400> 263  
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50  
tgacaccttc cctttcggcc ttgaggttcc cagcctggtg gccccaggac 100  
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tcctttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250  
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300  
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350  
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccgccattc 500  
 tggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550  
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600  
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650  
 ccatatgtta cctcatataa gtcacctgtc accactttag ataagagcac 700  
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750  
 aaactgcat agaaaaaccc gaagagtttg gaaagcacc agagagttgg 800  
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgca 850  
 acaggcactt cttagtgaac ccagcaaccc agcatataga gaagatattg 900  
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950  
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000  
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050  
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100  
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150  
 tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200  
 aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250  
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300  
 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350  
 atgtgttatg aacaattttc atatgcacta aaaaccta at ttaaaataaa 1400  
 attttggttc aggaaaaaa 1419

<210> 265  
 <211> 350  
 <212> PRT  
 <213> Homo sapiens

<400> 265  
 Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser  
 1 5 10 15  
 Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu  
 20 25 30  
 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg  
 35 40 45  
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50 55 60  
 Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys  
 65 70 75  
 Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu  
 80 85 90  
 Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly  
 95 100 105  
 Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro  
 110 115 120  
 Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala  
 125 130 135  
 Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu  
 140 145 150  
 Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val  
 155 160 165  
 Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro  
 170 175 180  
 Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu  
 185 190 195  
 Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys  
 200 205 210  
 Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp  
 215 220 225  
 Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala  
 230 235 240  
 Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu  
 245 250 255  
 Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala  
 260 265 270  
 Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro  
 275 280 285  
 Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile  
 290 295 300  
 Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp  
 305 310 315  
 Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val  
 320 325 330  
 Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala  
 335 340 345

Leu Leu Lys Val Tyr  
350

<210> 266  
<211> 2403  
<212> DNA  
<213> Homo sapiens

<400> 266  
cggctcgagc ggctcgagtg\_aagagcctct ccacggctcc tgcgcctgag 50  
acagctggcc tgacctcaa atcatccatc caccctgct gtcattctgtt 100  
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150  
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcaactg 200  
gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250  
tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt 300  
caggaatcag ttccatgctg tgggtccacct ctacagagat ggggaagact 350  
gggaatctaa gcagatgcca cagtatcgag ggagaactga gtttgtgaag 400  
gactccattg caggggggagc tgtctctcta aggctaaaaa acatcaactcc 450  
ctcggacatc ggctgtatg ggtgctgggt cagttcccag atttacgatg 500  
aggaggccac ctgggagctg cgggtggcag cactgggctc acttccctctc 550  
atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc 600  
ctcaggctgg tttccccagc ccacagccaa gtggaaaggc ccacaaggac 650  
aggatttgtc ttcagactcc agagcaaatg cagatgggta cagcctgtat 700  
gatgtggaga tctccattat agtccaggaa aatgctggga gcatattgtg 750  
ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggtattga 800  
taggagagac gtttttccag ccctcacctt ggcgctggtc ttctatttta 850  
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900  
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950  
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000  
gtgactctgg atccagagac ggctcaccgc aagctctgcg tttctgatct 1050  
gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100  
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaagcaggg 1150  
agacattact gggaggtgga cgtgggacaa aatgtagggg ggtatgtggg 1200  
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250



ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300  
 acattcaatc cccattttat cagcctcccc cccagcaccc ctcctacacg 1350  
 agtaggggtc ttcctggact atgaggggtg gaccatctcc ttcttcaata 1400  
 caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450  
 ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac 1500  
 tcccatattc atatgtccag tgtcctgggg atgagacaga gaagaccctg 1550  
 cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc 1600  
 ccgacaggtg gccccagctt cctctccgga gcctgcgcac agagagtcac 1650  
 gccccccact ctcctttagg gagctgaggt tcttctgccc tgagccctgc 1700  
 agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750  
 gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800  
 ttaggtttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850  
 cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900  
 tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950  
 tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000  
 accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050  
 aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100  
 ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150  
 gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200  
 gtccatatcc ctcattaaca cagacacaaa aattctaaat aaaattttta 2250  
 caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300  
 ggtttgtccc acaaatgcag agttgggtta atatttaa atcaaccagt 2350  
 gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400  
 aaa 2403

<210> 267  
 <211> 466  
 <212> PRT  
 <213> Homo sapiens

<400> 267  
 Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val  
 1 5 10 15  
 Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20 25 30  
 Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu  
 35 40 45  
 Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe  
 50 55 60  
 His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser  
 65 70 75  
 Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp  
 80 85 90  
 Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr  
 95 100 105  
 Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile  
 110 115 120  
 Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly  
 125 130 135  
 Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile  
 140 145 150  
 Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala  
 155 160 165  
 Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg  
 170 175 180  
 Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile  
 185 190 195  
 Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu  
 200 205 210  
 Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu  
 215 220 225  
 Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu  
 230 235 240  
 Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile  
 245 250 255  
 Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp  
 260 265 270  
 Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys  
 275 280 285  
 His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys  
 290 295 300  
 Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro  
 305 310 315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val  
 320 325 330  
 Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val  
 335 340 345  
 Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp  
 350 355 360  
 Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn  
 365 370 375  
 Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr  
 380 385 390  
 Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr  
 395 400 405  
 Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe  
 410 415 420  
 Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys  
 425 430 435  
 Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr  
 440 445 450  
 Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp  
 455 460 465

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
 ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg 50  
 tggtagagggc taggaaaaga gtttggttggg aaccctgggt tatcggcctc 100  
 gtcattcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150  
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350  
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
 agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450  
 tgtttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcaactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550  
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600  
 caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650  
 ctagcctgca gtgggatggg agtcatcgct gtggagcaac ctttaattaat 700  
 gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750  
 tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800  
 aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850  
 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900  
 aaatgcagta catagagttt gtctccctga tgcactctat gagtttcaac 950  
 caggtgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatggg 1000  
 tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050  
 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100  
 tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggatgactct 1150  
 ggaggaccac tggtagttc agatgctaga gatattctgg accttgctgg 1200  
 aatagtgage tggggagatg aatgtgcaaa acccaacaag cctgggtgttt 1250  
 atactagagt tacggccttg cgggactgga ttacttcaaa aactggtatc 1300  
 taagagacaa aagcctcatg gaacagataa catttttttt tggttttttg 1350  
 gtgtggaggc cattttttaga gatacagaat tggagaagac ttgcaaaaca 1400  
 gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450  
 ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc 1500  
 tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550  
 atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600  
 cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650  
 agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700  
 attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750  
 tcccctacat ttatttggca cagaaaagta ttaggtgttt ttcttagtgg 1800  
 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850  
 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900  
 tccagaaaga agccaagata tctccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000  
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050  
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100  
 cca 2103

<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269

Met Met Tyr Arg Pro Asp Val Val Arg-Ala Arg Lys Arg Val Cys  
 1 5 10 15  
 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile  
 20 25 30  
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
 35 40 45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
 50 55 60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
 65 70 75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
 80 85 90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
 95 100 105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
 110 115 120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
 125 130 135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
 140 145 150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
 155 160 165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
 170 175 180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
 185 190 195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
 200 205 210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
 215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro  
 230 235 240  
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys  
 245 250 255  
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys  
 260 265 270  
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser  
 275 280 285  
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp  
 290 295 300  
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly  
 305 310 315  
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg  
 320 325 330  
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro  
 335 340 345  
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly  
 350 355 360  
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly  
 365 370 375  
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly  
 380 385 390  
 Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly  
 395 400 405  
 Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys  
 410 415 420

Thr Gly Ile

<210> 270  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

<400> 270  
 gtcgaagggtt ataaaagctt ccagccaaac ggcattgaag ttgaagatac 50  
 aacctgacag cacagcctga gatcttgggg atccctcagc ctaacacca 100  
 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150  
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200  
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggtgttcc cctgcgacta 300  
 cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350  
 ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400  
 gacccgcccgc gcatgggaga agtgcgcatc gcggccgaag agggccgccc 450  
 agtgggtccac tgggtgtgccc ccttctcccc ggtcctccac tactggctgc 500  
 tgctttggga cggcagcgag gctgcgcaga aggggcccc gctgaacgct 550  
 acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600  
 cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650  
 ctggaggaga gggcctcgag ggggcccaca tccctgcctt cgggccttgc 700  
 agccgccttg cggtgccgcc caacccccgc actctgggtc acgcgccgct 750  
 cgggggtgggc acggccctgg ccctgctaag ctgtgccgcc ctgggtgtggc 800  
 acttctgcct gcgcgatcgc tggggctgcc cgccgagcgc cgccgcccga 850  
 gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900  
 cccacactgg ggcgtcagc ctggcccccg ggaaagagga aaaccgctg 950  
 cctccaggga gggctggacg gcgagctggg agccagcccc aggctccagg 1000  
 gccacggcgg agtcatggtt ctcaggactg agcgtttgtt taggtccggt 1050  
 acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100  
 ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150  
 ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271  
 <211> 238  
 <212> PRT  
 <213> Homo sapiens

<400> 271  
 Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe  
 1 5 10 15  
 Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu  
 20 25 30  
 Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala  
 35 40 45  
 Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys  
 50 55 60  
 Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly  
 65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<210> 272  
 <211> 2397  
 <212> DNA  
 <213> Homo sapiens

<400> 272  
 agagaaagaa gcgtctccag ctgaagccaa tgcagccctc cggctctccg 50  
 cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatc 100  
 cccaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgttt 150  
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200  
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250  
 acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300  
 tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350  
 aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac 400  
 cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450  
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500



aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550  
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg 600  
aaagccagga tgacaaatta tggattacct agatatcggg ggcttactca 650  
tgcttggaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700  
tactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750  
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gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000  
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acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150  
caaacttgtt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200  
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250  
tactattcta tgcttttaaa tgaggatgga aaagtttcat gtcataagtc 1300  
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350  
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400  
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450  
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actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900  
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000  
 cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050  
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 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200  
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250  
 cacagattat taaatttttt tacaagagta tagtatattt atttgaaatg 2300  
 ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350  
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<210> 273  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 273

Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr  
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 Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala  
 20 25 30  
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu  
 35 40 45  
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe  
 50 55 60  
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile  
 65 70 75  
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu  
 80 85 90  
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys  
 95 100 105  
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met  
 110 115 120  
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met  
 125 130 135  
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp  
 140 145 150  
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe  
 155 160 165  
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

	170		175		180
Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His	Gln		
	185		190		195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met		
	200		205		210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe		
	215		220		225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu		
	230		235		240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu	Pro		
	245		250		255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His		
	260		265		270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg		
	275		280		285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His	Phe		
	290		295		300
Glu Met Glu Glu	Leu				
	305				

<210> 274  
 <211> 2063  
 <212> DNA  
 <213> Homo sapiens

<400> 274  
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 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc 150  
 cttggggtga caatctcagc tccaggctac agggagaccc ggaggatcac 200  
 agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250  
 cgatgtcaaa cccctgcgca aaccccgtat ccccatggag accttcagaa 300  
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350  
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400  
 cgggcagcct ctccacttca tcccaggaa gcagctgtgt gacggagagc 450  
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 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550  
 ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600

tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650  
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 aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750  
 gctccctggg ctccctgcac tgtcttgctt gtgggaagag cctgaagacc 800  
 ccccggtgtg tgggtgggga ggaggcctct gtggattctt ggccttggca 850  
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 tccagccacc cactctgga tcattggatg gggctttacg aagcagaatg 1200  
 gagggagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250  
 agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300  
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg 1350  
 acagtgggtg gcccctgatg taccaatctg accagtggca tgtggtgggc 1400  
 atcgtagct ggggctatgg ctgcgggggc ccgagcacc caggagtata 1450  
 caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500  
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 ccctgcccac ctggggatcc ccaaagtca gacacagagc aagagtcccc 1600  
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 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850  
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900  
 tcttcacca tccccagcc tactagagca agaaaccagt tgtaatataa 1950  
 aatgcactgc cctactgttg gtatgactac cgttacctac tggtgtcatt 2000  
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caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp  
1 5 10 15

Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg  
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser  
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr  
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln  
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu  
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg  
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr  
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu  
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu  
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn  
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser  
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu  
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser  
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys  
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His  
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala  
245 250 255

265

Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys  
 260 265 270  
 Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp  
 275 280 285  
 Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr  
 290 295 300  
 Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro  
 305 310 315  
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn  
 320 325 330  
 Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val  
 335 340 345  
 Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu  
 350 355 360  
 Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val  
 365 370 375  
 Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser  
 380 385 390  
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys  
 395 400 405  
 Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr  
 410 415 420  
 Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu  
 425 430

<210> 276  
 <211> 3143  
 <212> DNA  
 <213> Homo sapiens

<400> 276  
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 gagcatggcc ctcccagccc tgggcctgga cccctggagc ctccctgggcc 150  
 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200  
 ggaggcgggc aggggcccac gccaggggtc agatactatg caggggatga 250  
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 ctctgctcct gagtggtgat ggaaatactc tctacgtggg ggctcgagaa 350  
 gccattctgg ccttgatata ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450  
agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctgggt 500  
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550  
tgcttgtacc ttcattgaac ttcaagattc ctacctgttg cccatctcgg 600  
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aagaagtcct ggctgtcccc aactccatcc tggagctccc ctgccccac 1850

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 agagactggt tattttttat taaaaatata aggcttaaaa aaa 3143

<210> 277  
 <211> 761  
 <212> PRT  
 <213> Homo sapiens  
 <400> 277



Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly  
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 Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr  
 20 25 30  
 Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr  
 35 40 45  
 Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly  
 50 55 60  
 Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr  
 65 70 75  
 Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln  
 80 85 90  
 Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala  
 95 100 105  
 Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn  
 110 115 120  
 Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn  
 125 130 135  
 Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala  
 140 145 150  
 Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser  
 155 160 165  
 Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro  
 170 175 180  
 Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser  
 185 190 195  
 Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg  
 200 205 210  
 Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg  
 215 220 225  
 Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr  
 230 235 240  
 Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp  
 245 250 255  
 Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys  
 260 265 270  
 Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr  
 275 280 285  
 Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

290 295 300  
 Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro  
 305 310 315  
 Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val  
 320 325 330  
 Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp  
 335 340 345  
 Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu  
 350 355 360  
 Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg  
 365 370 375  
 Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr  
 380 385 390  
 Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr  
 395 400 405  
 Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val  
 410 415 420  
 Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr  
 425 430 435  
 Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly  
 440 445 450  
 Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp  
 455 460 465  
 Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala  
 470 475 480  
 Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala  
 485 490 495  
 Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg  
 500 505 510  
 Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu  
 515 520 525  
 Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg  
 530 535 540  
 Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser  
 545 550 555  
 Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala  
 560 565 570  
 Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala  
 575 580 585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu  
 590 595 600  
 Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln  
 605 610 615  
 Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly  
 620 625 630  
 Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln  
 635 640 645  
 Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His  
 650 655 660  
 Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala  
 665 670 675  
 Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu  
 680 685 690  
 Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser  
 695 700 705  
 Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu  
 710 715 720  
 Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His  
 725 730 735  
 Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp  
 740 745 750  
 Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala  
 755 760

<210> 278  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 278  
 ctgctggtga aatctggcgt ggag 24

<210> 279  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 279  
gtctggtcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 280  
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

B1  
<400> 281  
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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250  
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300  
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tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450  
ggatatcatg gattccttaa agaattgagaa cttcgacatg gtgatagttg 500  
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550  
tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600  
aatccccttg tcttatgttc cagtattccg ttccttgctg actgatcaca 650  
tggaacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700  
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agttgtggtt cattaactct gactttgcct ttgattttgc tcgacctctg 850  
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B1

<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro  
 1 5 10 15  
 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr  
 20 25 30  
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile  
 35 40 45  
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg  
 50 55 60  
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln  
 65 70 75  
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys  
 80 85 90  
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly  
 95 100 105  
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln  
 110 115 120  
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys  
 125 130 135  
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys  
 140 145 150  
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile  
 155 160 165  
 Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro  
 170 175 180  
 Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met  
 185 190 195  
 Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe  
 200 205 210  
 Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile  
 215 220 225  
 Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu  
 230 235 240  
 Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe  
 245 250 255  
 Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

	260		265		270
Leu Met Glu Lys	Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn			
	275	280			285
Phe Ile Ala Lys	Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu			
	290	295			300
Gly Ser Met Val	Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu			
	305	310			315
Met Asn Asn Ala	Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys			
	320	325			330
Cys Gln Cys Ser	His Trp Pro Lys Asp	Val His Leu Ala Ala Asn			
	335	340			345
Val Lys Ile Val	Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His			
	350	355			360
Pro Ser Ile Arg	Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile			
	365	370			375
Met Glu Ala Ile	Gln His Gly Val Pro	Met Val Gly Ile Pro Leu			
	380	385			390
Phe Gly Asp Gln	Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys			
	395	400			405
Phe Gly Val Ser	Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu			
	410	415			420
Ala Leu Lys Met	Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser			
	425	430			435
Ala Ala Val Ala	Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser			
	440	445			450
Pro Thr Gln Arg	Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr			
	455	460			465
Gly Gly Ala Thr	His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp			
	470	475			480
His Glu Gln Tyr	Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu			
	485	490			495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala			
	500	505			510
Val Trp Trp Leu	Arg Gly Ala Arg Lys	Val Lys Glu Thr			
	515	520			

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 283  
tgcctttgct cacctacccc aagg 24

<210> 284  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 284  
tcaggctggt ctccaaagag aggg 24

<210> 285  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 285  
cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 286  
gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50  
ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100  
cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150  
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
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gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc aggggtgccgg cggtgagaat 400  
ccagggagag gaggcgaaac agaagagggg cagaagaccg gggcacttgt 450



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 gggagcagcc ctgggagagg cccccctgg gcgagtggca tttgctgcgg 700  
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750  
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 ccgggcctct ggctccttcg tagcccctgt ccgggggtgc tacagcttcc 850  
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900  
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950  
 gacccgggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000  
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050  
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100  
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 cccagaaac agcagaggca ggagagagac tccctctggc tcctatcca 1200  
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250  
 gagctgtggc atctccagac caggccttcc caccaccca ccccagtta 1300  
 ccctcccagc cacctgctgc atctgttccct gcctgcagcc ctaggatcag 1350  
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 ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttcctgtgag gaaagccagc atcacggatc 1550  
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B1

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
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 cattccttca gacctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
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 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250  
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170		175		180									
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser
				185					190					195

Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu
				200					205

<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
 aggcagccac cagctctgtg ctac 24

B1

<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
 cagagaggga agatgaggaa gccagag 27

<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
 ctgtgctact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50  
 tagccgccca gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100  
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu  
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 Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro  
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 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser  
 35 40 45  
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn  
 50 55 60  
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln  
 65 70 75  
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile  
 80 85 90  
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu  
 95 100 105  
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly  
 110 115 120  
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr  
 125 130 135  
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu  
 140 145 150  
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile  
 155 160 165  
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu  
 170 175 180  
 Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu  
 185 190 195  
 Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser  
 200 205 210  
 Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu  
 215 220 225  
 Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly  
 230 235 240  
 Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr  
 245 250 255  
 Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260 265 270  
 Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr  
 275 280 285  
 Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln  
 290 295 300  
 Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His  
 305 310 315  
 Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr  
 320 325 330  
 Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro  
 335 340 345  
 Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr  
 350 355 360  
 Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr  
 365 370 375  
 Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn  
 380 385

<210> 293  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 293  
 gctgacctgg ttcccatcta ctcc 24

<210> 294  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 294  
 cccacagaca cccatgacac ttcc 24

<210> 295  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 295  
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

B1  
<400> 296  
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ccgacgcagg gccggggccg gccaggggcc gaggagcgcg gcggccagag 100  
cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
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cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
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 aaaaacccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500  
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 aatcaaagtg tcaaatagca aagaatcttg aaagcagcaa gagatgagca 1850  
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 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000  
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050  
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100  
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 gtgatcccaa gtagcttgga ttgtaaacat gcaccacat gcctggctaa 2350  
 tttttgtatt tttagtagag acgtgttagc caggctggtc tcgatctcct 2400  
 gacctcaagt gaccacctgc ctgagcctcc caaagtactg ggattacagg 2450  
 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500  
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550  
 cctttttaaa tttttattat ttatttatat atttattttg agacagggtc 2600



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 accctgtctc 3060

<210> 297  
 <211> 368  
 <212> PRT  
 <213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe  
 170 175 180  
 Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys  
 185 190 195  
 Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly  
 200 205 210  
 Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val  
 215 220 225  
 Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu  
 230 235 240  
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val  
 245 250 255  
 Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala  
 260 265 270  
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln  
 275 280 285  
 Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys  
 290 295 300  
 Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala  
 305 310 315  
 Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe  
 320 325 330  
 Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val  
 335 340 345  
 Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu  
 350 355 360  
 Glu Pro Gly Arg Trp Arg Leu Gln  
 365

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 298  
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<210> 299  
 <211> 21  
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150  
tcagtttgct ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200  
cggccctggg ttagaaggga aggaagata aacttttata caaatgggga 250  
tagctggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300  
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400  
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500  
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
ctggcctgac agaatctcat cttgtttaat gctctcataa gaccacttgt 650  
ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700  
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 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900  
 cgttgactgt gcttgtgaat tatctgggga tgcaggctcct gattcagtag 950  
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 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgata 1100  
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 tctgtactaa aaatacaca attagctggg catggtggca catgcctgta 1200  
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250  
 gcggagggtt cagtgaagcc agatcaggcc actgtattcc aaccagggtg 1300  
 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5					10					15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303

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 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100  
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200  
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300  
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350  
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400  
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450  
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 ggcgatggct cccactgccc aggcacacgc cttgctgtag tcaatcactg 550  
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600  
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tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
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 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500  
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550  
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 aggcattggt gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650  
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750  
 aattatgggt atttgtaa 1768

<210> 304  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
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 1 5 10 15  
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu  
 20 25 30  
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly  
 35 40 45  
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly  
 50 55 60  
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro  
 65 70 75  
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala  
 80 85 90  
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly  
 95 100 105  
 Arg Arg Arg Asp

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305

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 tgtcactgcc tcccgccgcc tctgtcccgc gccatgaccc agccggtgcc 100  
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 ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
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 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgagag 350  
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 cgctgcccgc ggacgggagc gtggtgacct gcgaggtgga cgcgcagccc 500  
 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550  
 cgacctccgg ctgaagcccg ccttggagac cctggacgag ctgctggcgg 600  
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 caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900  
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
 Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala  
 1 5 10 15  
 Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe  
 20 25 30  
 Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys  
 35 40 45  
 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser  
 50 55 60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu  
 65 70 75  
 Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln  
 80 85 90  
 Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys  
 95 100 105  
 Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu  
 110 115 120  
 Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val  
 125 130 135  
 Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala  
 140 145 150  
 Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu  
 155 160 165  
 Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp  
 170 175 180  
 Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr  
 185 190 195  
 Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val  
 200 205 210  
 Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly  
 215 220 225  
 Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg  
 230 235 240  
 Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly  
 245 250 255  
 Leu Thr Leu Ala Phe Lys Ile  
 260

<210> 307  
 <211> 2272  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
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 ctctcgccgt cagcatgccca cacgccttca agcccgggga cttggtgttc 100  
 gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150  
 ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200  
 gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250



aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
 agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc 350  
 cgccagttag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400  
 ggcagttagc ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450  
 agcggttaacc gccacagctg ccagcgacag gatggagagc gactcagact 500  
 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550  
 aagatgtcgg tctcgaaacg agcccgaag gcctccagcg acctggatca 600  
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 cgggcgccac ggagggggccc tctgggggga cggaaaaaaa agaaggcgcc 750  
 gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaaagcctg 800  
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 cctctgactc cgagcccag gccgagctgg agagagaggc caagaaatca 1300  
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 aggtggagcg gacccggaag cgggtccgagg gcttctcgat ggacaggaag 1450  
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 cagttagatc aagtttgccc taaaggtcga cagcccgac gtgaagaggt 1550  
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 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650  
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tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750  
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ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900  
agcgagagg acaaggagca cgaggagggt cgggactcgg aggagggggc 1950  
aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000  
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gccccgccc gagctcaggc tgcccctctc cttccccggc tcgcaggaga 2150  
gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttcctt 2200  
gggttttttt ttcctgccta atttctgtga tttccaacca acatgaaatg 2250  
actataaacg gttttttaat ga 2272

<210> 308  
<211> 671  
<212> PRT  
<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

140 145 150  
 Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser  
 155 160 165  
 Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala  
 170 175 180  
 Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu  
 185 190 195  
 Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala  
 200 205 210  
 Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys  
 215 220 225  
 Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser  
 230 235 240  
 Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser  
 245 250 255  
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val  
 260 265 270  
 Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro  
 275 280 285  
 Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser  
 290 295 300  
 Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu  
 305 310 315  
 Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg  
 320 325 330  
 Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln  
 335 340 345  
 Glu Lys Glu Glu Lys Glu Arg Arg Arg Glu Arg Ala Asp Arg Gly  
 350 355 360  
 Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg  
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 Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly  
 380 385 390  
 Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu  
 395 400 405  
 Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser  
 410 415 420  
 Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg  
 425 430 435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr  
 440 445 450  
 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys  
 455 460 465  
 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser  
 470 475 480  
 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg  
 485 490 495  
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser  
 500 505 510  
 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys  
 515 520 525  
 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala  
 530 535 540  
 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile  
 545 550 555  
 Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys  
 560 565 570  
 Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala  
 575 580 585  
 Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala  
 590 595 600  
 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu  
 605 610 615  
 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg  
 620 625 630  
 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro  
 635 640 645  
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 650 655 660  
 Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser  
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<210> 309  
 <211> 3871  
 <212> DNA  
 <213> Homo sapiens

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 tcagagtact tcagccctat aaaaaactc acatatatgt gtgtggaact 550  
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 tcactcctgg agaattgtat aggaatttgg agaggtgcat tatttctttc 3000

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tggccactgg ggttaaattt agtgtactac aacattgatt tactgaagg 3050  
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 cacagagaga agttggtgct tagttatgtg ttttttagag tatatactaa 3150  
 gctctacagg gacagaatgc ttaataaata ctttaataag atatgggaaa 3200  
 atattttaat aaaacaagga aaacataatg atgtataatg catcctgatg 3250  
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 cacaataaaa gtgagagtaa tgtaatggag ctcttttcac taggggtataa 3400  
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 aactgctagc aaaatctgag gaaacataaa ttcttctgaa gaatcatagg 3500  
 aagagtagac attttattta taaccaatga tatttcagta tatattttct 3550  
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 gagaaaacaa tatataacac acagagaatt aagaaaatga catttctggg 3700  
 gagtggggat atatatttgt tgaataacag aacgagtgt aatttttaac 3750  
 aacggaaagg gttaaattaa ctctttgaca tcttcactca accttttctc 3800  
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 ataaataagc ctgctacatg t 3871

<210> 310  
 <211> 777  
 <212> PRT  
 <213> Homo sapiens

<400> 310  
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 Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu  
 35 40 45  
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro  
 50 55 60  
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu  
 65 70 75  
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

	80		85		90
Phe Leu Leu Ser	Leu 95	Val Asp Leu Asn	Lys 100	Asn Phe Lys Lys	Ile 105
Tyr Trp Pro Ala	Ala 110	Lys Glu Arg Val	Glu 115	Leu Cys Lys Leu	Ala 120
Gly Lys Asp Ala	Asn 125	Thr Glu Cys Ala	Asn 130	Phe Ile Arg Val	Leu 135
Gln Pro Tyr Asn	Lys 140	Thr His Ile Tyr	Val 145	Cys Gly Thr Gly	Ala 150
Phe His Pro Ile	Cys 155	Gly Tyr Ile Asp	Leu 160	Gly Val Tyr Lys	Glu 165
Asp Ile Ile Phe	Lys 170	Leu Asp Thr His	Asn 175	Leu Glu Ser Gly	Arg 180
Leu Lys Cys Pro	Phe 185	Asp Pro Gln Gln	Pro 190	Phe Ala Ser Val	Met 195
Thr Asp Glu Tyr	Leu 200	Tyr Ser Gly Thr	Ala 205	Ser Asp Phe Leu	Gly 210
Lys Asp Thr Ala	Phe 215	Thr Arg Ser Leu	Gly 220	Pro Thr His Asp	His 225
His Tyr Ile Arg	Thr 230	Asp Ile Ser Glu	His 235	Tyr Trp Leu Asn	Gly 240
Ala Lys Phe Ile	Gly 245	Thr Phe Phe Ile	Pro 250	Asp Thr Tyr Asn	Pro 255
Asp Asp Asp Lys	Ile 260	Tyr Phe Phe Phe	Arg 265	Glu Ser Ser Gln	Glu 270
Gly Ser Thr Ser	Asp 275	Lys Thr Ile Leu	Ser 280	Arg Val Gly Arg	Val 285
Cys Lys Asn Asp	Val 290	Gly Gly Gln Arg	Ser 295	Leu Ile Asn Lys	Trp 300
Thr Thr Phe Leu	Lys 305	Ala Arg Leu Ile	Cys 310	Ser Ile Pro Gly	Ser 315
Asp Gly Ala Asp	Thr 320	Tyr Phe Asp Glu	Leu 325	Gln Asp Ile Tyr	Leu 330
Leu Pro Thr Arg	Asp 335	Glu Arg Asn Pro	Val 340	Val Tyr Gly Val	Phe 345
Thr Thr Thr Ser	Ser 350	Ile Phe Lys Gly	Ser 355	Ala Val Cys Val	Tyr 360
Ser Met Ala Asp	Ile 365	Arg Ala Val Phe	Asn 370	Gly Pro Tyr Ala	His 375

300

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Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile  
 380 385 390  
 Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro  
 395 400 405  
 Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe  
 410 415 420  
 Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala  
 425 430 435  
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr  
 440 445 450  
 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp  
 455 460 465  
 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val  
 470 475 480  
 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu  
 485 490 495  
 Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu  
 500 505 510  
 Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly  
 515 520 525  
 Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala  
 530 535 540  
 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp  
 545 550 555  
 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala  
 560 565 570  
 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp  
 575 580 585  
 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val  
 590 595 600  
 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro  
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 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly  
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 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys  
 635 640 645  
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser  
 650 655 660  
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

665										670					675				
Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu					
				680					685					690					
Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu					
				695					700					705					
Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu					
				710					715					720					
Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp					
				725					730					735					
His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp					
				740					745					750					
Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His					
				755					760					765					
Arg	Asp	Leu	Asp	Glu	Leu	Pro	Arg	Ala	Val	Ala	Thr								
				770					775										

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<210> 311  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 311  
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<210> 312  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 312  
 gcttggacat gtaccaggcc gtgg 24

<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 313  
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<210> 314  
<211> 3934  
<212> DNA  
<213> Homo sapiens

<400> 314  
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agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150  
ctcagcagtt tcagccagca gggactgac aggtgtgtgt cctggagtgg 200  
ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250  
cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300  
gggtgagggtg ggggggcaca ggtgtcatgt gcaccttctt gtctcagcaa 350  
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 tttcttgtct ttatctaata aactcaatat taag 3934

<210> 315  
 <211> 370  
 <212> PRT  
 <213> Homo sapiens

<400> 315  
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 1 5 10 15

Val Phe Pro Pro Thr Pro Val Leu Cys Leu Pro Asn Gln Val Leu  
 20 25 30  
 Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala  
 35 40 45  
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg  
 50 55 60  
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu  
 65 70 75  
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala  
 80 85 90  
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser  
 95 100 105  
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp  
 110 115 120  
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu  
 125 130 135  
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro  
 140 145 150  
 Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp  
 155 160 165  
 Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu  
 170 175 180  
 Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu  
 185 190 195  
 Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser  
 200 205 210  
 Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu  
 215 220 225  
 Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln  
 230 235 240  
 Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu  
 245 250 255  
 Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly  
 260 265 270  
 Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu  
 275 280 285  
 Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu  
 290 295 300  
 Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala

	305		310		315
Pro Thr Ser Val	Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro	Gly		
	320	325	330		
Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met	Ala Pro		
	335	340	345		
Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala	Lys Ala		
	350	355	360		
Pro Asp Pro Gly	His Pro Asp Pro	Leu Thr			
	365	370			

<210> 316  
 <211> 4407  
 <212> DNA  
 <213> Homo sapiens

<400> 316  
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 cagccctgac cttccgagag gagcagtgtg ctgcctacaa ccaccgcacc 2200  
 gacctcttca agagcttccc agggcccatg gactgggttc ctcgctacac 2250  
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 tccccggaca gtcctcgggt ctgtgtccag ggccgatgca tccatgctgg 2400



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 cagcaattct cctgcctcag cctcccagat agctgagatt ataggcacct 3850

accaccaagc ccggctaatt tttgtatttt tagtagagac ggggtttcac 3900  
catgttggcc aggctggtct cgaactcctg accttaggtg atccactcgc 3950  
cttcatctcc caaagtgctg ggattacagg cgtgagccac cgtgcctggc 4000  
cacgccaac taatttttgt attttttagta gagacagggt ttcacatgt 4050  
tggccaggct gctcttgaac tcctgacctc aggtaatcga cctgcctcgg 4100  
cctcccaaag tgctgggatt acaggtgtga gccaccacgc ccggtacata 4150  
ttttttaaat tgaattctac tatttatgtg atccttttgg agtcagacag 4200  
atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250  
ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400  
aaggaaa 4407

<210> 317  
<211> 837  
<212> PRT  
<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg	1	5	10	15
Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro	20	25	30	
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	35	40	45		
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	50	55	60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	65	70	75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	80	85	90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	95	100	105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	110	115	120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	125	130	135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu				

140 145 150  
 Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu  
 155 160 165  
 Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile  
 170 175 180  
 Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn  
 185 190 195  
 Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala  
 200 205 210  
 Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val  
 215 220 225  
 Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg  
 230 235 240  
 Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His  
 245 250 255  
 Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val  
 260 265 270  
 Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala  
 275 280 285  
 Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn  
 290 295 300  
 Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu  
 305 310 315  
 Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu  
 320 325 330  
 Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys  
 335 340 345  
 Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala  
 350 355 360  
 His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys  
 365 370 375  
 Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val  
 380 385 390  
 Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser  
 395 400 405  
 Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr  
 410 415 420  
 Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro  
 425 430 435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln  
 440 445 450  
 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro  
 455 460 465  
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala  
 470 475 480  
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys  
 485 490 495  
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp  
 500 505 510  
 Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro  
 515 520 525  
 Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val  
 530 535 540  
 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly  
 545 550 555  
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn  
 560 565 570  
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu  
 575 580 585  
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe  
 590 595 600  
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro  
 605 610 615  
 Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr  
 620 625 630  
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser  
 635 640 645  
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala  
 650 655 660  
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys  
 665 670 675  
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly  
 680 685 690  
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile  
 695 700 705  
 Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro  
 710 715 720  
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp					
	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr					
	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro					
	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg					
	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro					
	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu					
	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys					
	830		835		

<210> 318  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
 ccctgaagct gccagatggc tcc 23

<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctctt cggtgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321  
<211> 1197  
<212> DNA  
<213> Homo sapiens

B1  
<400> 321  
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgtttt 200  
gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg 350  
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
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gacccgtcac gccagacaag caagtgagga agaacttcca ataatgact 800  
atactgaaaa tggaatagaa tttgatccca tgctgga'tga gagaggttat 850  
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atataataaa tgc'atgctat tcaatgaatt tctgcctatg aggcattctg 1100  
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150  
tg'ttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322

Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu  
 1 5 10 15  
 Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys  
 20 25 30  
 Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val  
 35 40 45  
 Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys  
 50 55 60  
 Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys  
 65 70 75  
 Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe  
 80 85 90  
 Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe  
 95 100 105  
 Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys  
 110 115 120  
 Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro  
 125 130 135  
 Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe  
 140 145 150  
 Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn  
 155 160 165  
 Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn  
 170 175 180  
 Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu  
 185 190 195  
 Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala  
 200 205 210  
 Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro  
 215 220 225  
 Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu  
 230 235 240  
 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe  
 245 250 255  
 Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg  
 260 265 270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
 275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
 290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
 305 310 315

Arg Val

<210> 323  
 <211> 1174  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
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 ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150  
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 accaacaacc tcacggccgt gtcctacctg aaagggtctt ggatggagtg 250  
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 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950  
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000



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 atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100  
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150  
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 324

Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe  
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 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp  
 20 25 30  
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser  
 35 40 45  
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly  
 50 55 60  
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu  
 80 85 90  
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu  
 110 115 120  
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala  
 125 130 135  
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro  
 140 145 150  
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr  
 155 160 165  
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu  
 170 175 180  
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln  
 185 190 195  
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala  
 200 205 210  
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val  
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
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 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100  
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccgggt 150  
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200  
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250  
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300  
 gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcata 350  
 gtcttgggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400  
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 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550  
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 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800  
 aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta 850  
 tccttccaag cagcactatg tgtaatgctc taagacctct cagcacgggc 900  
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950  
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000  
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050  
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100  
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150  
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
 cccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatggtatt 1300  
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350  
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
 cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450  
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500  
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550  
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600  
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctacccccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850  
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100  
 aggttaaaac taattcttta a 2121

<210> 326  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile  
 1 5 10 15  
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp  
 20 25 30  
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln  
 35 40 45  
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe  
 50 55 60  
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met  
 65 70 75  
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80 85 90  
 Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg  
 95 100 105  
 Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr  
 110 115 120  
 Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly  
 125 130 135  
 Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser  
 140 145 150  
 Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val  
 155 160 165  
 Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val  
 170 175 180  
 Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala  
 185 190 195  
 Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser  
 200 205 210  
 Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe  
 215 220 225  
 Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile  
 230 235 240  
 Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro  
 245 250 255  
 Ser Lys His Asp Tyr Val  
 260

<210> 327  
 <211> 2010  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150  
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200  
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250  
 tgaattgcgt gaggcaggct aacatcagga tgcagtcaa aatctatgat 300  
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400  
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450  
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500  
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550  
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600  
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650  
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
 atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750  
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850  
 caaagaaact ttgatttact gttcttaact gcctaattct aattacagga 900  
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattatth tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgt acatttatat ctcacataga gacatgctta 1150  
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450  
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500  
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650  
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700  
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750  
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

B1

atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850  
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900  
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000  
 ttttctaatt 2010

<210> 328  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly  
 1 5 10 15  
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp  
 20 25 30  
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn  
 35 40 45  
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile  
 50 55 60  
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met  
 80 85 90  
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu  
 110 115 120  
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile  
 125 130 135  
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn  
 140 145 150  
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu  
 155 160 165  
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala  
 170 175 180  
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr  
 185 190 195  
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His  
 200 205 210

B1

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

<400> 329

tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50  
 ctgggctggg tgaatggcct ggtctcctgt gccctgcca tgtggaaggt 100  
 gaccgctttc atcggcaaca gcatcgtggt ggcccaggtg gtgtgggagg 150  
 gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
 cctctgtgtc atgcacctcc ttgtggccct gttcggcttg ctggtctacc 300  
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
 cgctgggtgc tcacctctgg gattgtcttt gtcatctcag gggctctgac 400  
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450  
 accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500  
 ttgggctggg cggcctcagg ccttttgctg ctgggtgggg ggttgctgtg 550  
 ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600  
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650  
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700  
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750  
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800  
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850  
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900  
 tctggatctt gacatgcca tcttagaagc cagtcaagct atggaactaa 950  
 tgcgagggt gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000  
 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050  
 gctgcccccc atcctactca ggtctctgga gctcctctct tcaccctgg 1100  
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150  
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200  
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250

B1

gccccctcg tctcaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu  
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp  
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val  
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly  
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln  
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val  
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr  
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr  
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro  
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro  
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr  
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu  
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His  
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly  
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val  
215 220

<210> 331

<211> 1160

<212> DNA



<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50  
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100  
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150  
gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggg 200  
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250  
ggaagggtc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300  
gcaagttcta tagctccttg ttggctctcc cgctgccct ggaaacagcc 350  
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg cctgcttat 400  
tggcatctgt ggcatagaag aggtccagtg cacaggctct aacgagaggg 450  
ccaaagcata ctttctggga acttcaggag tcctcttcat cctgacgggt 500  
atcttcgttc tgattccggt gagctggaca gccaataata tcatcagaga 550  
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600  
cacttttcct tggctgggca agcgtgctg tcctcttcat tggagggggg 650  
ctgctttgtg gatcttctg ctgcaacaga aagaagcaag ggtacagata 700  
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750  
caatgcttag taagacctcc accagttatg tctaatacct ctttttggct 800  
ccaagtatgg actatgggtca atgtttttta taaagtctg ctagaaactg 850  
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900  
cgaaagtttc aatttggtac tgggtggtagg aatgaaaatg acttacttgg 950  
acattctgac ttcaggtgta ttaaatacat tgactattgt tggacccaat 1000  
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050  
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100  
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150  
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu	Leu Ala Leu Pro Pro	Ala Leu Glu Thr Ala	Arg
	20	25	30
Ala Leu Met Cys	Val Ala Val Ala Leu	Ser Leu Ile Ala Leu	Leu
	35	40	45
Ile Gly Ile Cys	Gly Met Lys Gln Val	Gln Cys Thr Gly Ser	Asn
	50	55	60
Glu Arg Ala Lys	Ala Tyr Leu Leu Gly	Thr Ser Gly Val Leu	Phe
	65	70	75
Ile Leu Thr Gly	Ile Phe Val Leu Ile	Pro Val Ser Trp Thr	Ala
	80	85	90
Asn Ile Ile Ile	Arg Asp Phe Tyr Asn	Pro Ala Ile His Ile	Gly
	95	100	105
Gln Lys Arg Glu	Leu Gly Ala Ala Leu	Phe Leu Gly Trp Ala	Ser
	110	115	120
Ala Ala Val Leu	Phe Ile Gly Gly Gly	Leu Leu Cys Gly Phe	Cys
	125	130	135
Cys Cys Asn Arg	Lys Lys Gln Gly Tyr	Arg Tyr Pro Val Pro	Gly
	140	145	150
Tyr Arg Val Pro	His Thr Asp Lys Arg	Arg Asn Thr Thr Met	Leu
	155	160	165
Ser Lys Thr Ser	Thr Ser Tyr Val		
	170		

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50  
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100  
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150  
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200  
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250  
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300  
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350  
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400  
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr  
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccgttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

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tggccctgac cgggctggcg ctgctcctgc tctgtgtctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccagagtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaatt 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
gaagagttaa aacaacacat gtaaagcct tttgatattt catgggaatg 700  
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336

Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly  
1 5 10 15  
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser  
20 25 30  
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337

cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50  
agccggggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100  
tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150  
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200  
gaccactgc ccagccgtc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300  
 ccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350  
 gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400  
 gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450  
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500  
 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550  
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600  
 tgtccacgag agtcggtccc ccaaattccc cctgcccgcc ggggtccgag 650  
 cccggcccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700  
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750  
 ttcccctgac cgccactctg ggccctggcg gcttcaccct gctcctcagt 800  
 ctccctggcct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850  
 agcgtcgcgc gccctccgcg accttgctcc ccgcgccgcg gcgggagctg 900  
 ctgcctgccc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950  
 gccagccct gcgcgcgaga ggactcccgc gactggcgga ggccccgccc 1000  
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050  
 cgcactggga gtgggctcct cggggctcggg catctgctgt cgctgcctcg 1100  
 gccccgggca gagccgggcc gccccggggg cccgtcttag tgttctgccg 1150  
 gaggaccag ccgcctccaa tccctgacag ctccctgggc tgagttgggg 1200  
 acgccaggtc ggtgggaggc tgggtgaagg gagcggggag gggcagagga 1250  
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300  
 aaaaaaaaaa 1310

<210> 338  
 <211> 246  
 <212> PRT  
 <213> Homo sapiens

<400> 338  
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe  
 1 5 10 15  
 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
 20 25 30  
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
 35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp  
 50 55 60  
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg  
 65 70 75  
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr  
 80 85 90  
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu  
 95 100 105  
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp  
 110 115 120  
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly  
 125 130 135  
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly  
 140 145 150  
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys  
 155 160 165  
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro  
 170 175 180  
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile  
 185 190 195  
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu  
 200 205 210  
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala  
 215 220 225  
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala  
 230 235 240  
 Phe Ala Met Tyr Arg Pro  
 245

<210> 339  
 <211> 849  
 <212> DNA  
 <213> Homo sapiens

<400> 339  
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 caagacccta agaaccatca gccctcagct gcacctcctc ccctccaagg 150  
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200  
 tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag gggttactccc tgagtgactg gctgtgcctg 300  
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400  
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500  
gtccggagca cgggggatga acaactgggt agaattggagg ttgcactgtt 550  
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600  
aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700  
ccttcccatt tacaactaaa actgaccaga gcccagga taaatggttt 750  
tcttggttc ctccttactc ccactctggac ccagtcccct ggttctgtc 800  
tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 340  
Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala  
1 5 10 15  
Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val  
20 25 30  
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
35 40 45  
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
50 55 60  
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
65 70 75  
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
80 85 90  
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
95 100 105  
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
110 115 120  
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
125 130 135  
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 341  
ccctccaagg atgacaaagg cgc 23

<210> 342  
<211> 29  
<212> DNA  
<213> Artificial

B1  
<220>  
<221> Artificial Sequence  
<222> 1-29  
<223> Synthetic construct.

<400> 342  
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 343  
atctcaggcg gcatcctgtc agcc 24

<210> 344  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 344  
gtggatgcct gcaagaaggt tggg 24

<210> 345  
<211> 45  
<212> DNA  
<213> Artificial



<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

B1  
<400> 346  
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actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350  
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400  
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450  
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500  
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550  
ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600  
aagccagcaa gcacagccct gaagccagggt accgcctgga ctttggggaa 650  
tcccaggatt gggactgga agctgaggat gaggggtgaag agtacagccc 700  
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750  
tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800  
ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850  
cccaaagagg gactgggggg ctgatgagga cggggagggtg tctgaagaag 900  
aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950  
agtgcccgca tccccctcca gagggctctg cccgaggtgc ggcaccact 1000  
gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050  
tctgtttcca tgatgaggcc tgggtccactc tctgcggac tgtacacagc 1100

atcctcgaca cagtgtcccag ggccttcctg aaggagatca tcctcgtgga 1150  
 cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200  
 ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250  
 atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300  
 cttcatggat gccactgcg agtgccaccc aggctggctg gagcccctcc 1350  
 tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400  
 gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450  
 tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500  
 atgtgaggaa ggccctccag tccccataa gcccacacag gagccctgtg 1550  
 gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600  
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 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
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 atatatttca tgaagctgat ccttttgtgt gtgtgctcct tgtgttagga 2500  
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B1

tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln  
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Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val  
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr  
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp  
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly  
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu  
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg  
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile  
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp  
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr  
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala  
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu  
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val  
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr  
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu  
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser  
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu  
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly  
 260 265 270  
 Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His  
 275 280 285  
 Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile  
 290 295 300  
 Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile  
 305 310 315  
 Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg  
 320 325 330  
 Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro  
 335 340 345  
 Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg  
 350 355 360  
 Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr  
 365 370 375  
 Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly  
 380 385 390  
 Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly  
 395 400 405  
 Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln  
 410 415 420  
 Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg  
 425 430 435  
 Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu  
 440 445 450  
 Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala  
 455 460 465  
 Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu  
 470 475 480  
 Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu  
 485 490 495  
 Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His  
 500 505 510  
 Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp  
 515 520 525  
 Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg  
 530 535 540  
 Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 350  
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

<400> 351

cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50  
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100  
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200  
caggggaggc ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250  
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300  
cctggcactg cacccccagc caccocatca ggctttgagg aggggccgcc 350  
ctcatcccaa tacccttggg ctatcgtgtg gggcccacc gtgtctcgag 400  
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatggt 450  
tttgagccc ctcatgggct cgcaacccca caccccaact cagactccat 500  
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550  
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cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700  
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caactctgcc ctcttaacct tgattccccc tctttgtctt gaacttcccc 1200  
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ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350  
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 cacccttggt cactcacatg aaagccttgc acactcacct ccaccttcac 1550  
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 tctgacagat gggttttggg gagtcgcctg ctgcactaca tgagaaagg 2050  
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 tcaaataaag cctttgcaag ataa 2524

<210> 352  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
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Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
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 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135  
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
 140 145 150  
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
 155 160 165  
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
 170 175 180  
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
 185 190 195  
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
 200 205 210  
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
 215 220 225  
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
 230 235 240

Leu Pro Lys

<210> 353  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 353  
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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350  
 tcgccgcctt gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser,  
 1 5 10 15  
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
 20 25 30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
 35 40 45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
 50 55 60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
 65 70 75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
 80 85 90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
 95 100 105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
 110 115 120  
 Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
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 gttggccggc ggcgggcccgg gacgggcatg gccctgctgc tgtgcctggg 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150  
 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200  
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300  
 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
 taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400  
 catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
 acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500  
 agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
 agtagccccc agaggcgctg ggagtgttgc caccgccctc ccctgaagtt 600  
 tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggccc 650  
 atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
 tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750  
 acgtcgctg ctttggctat aactgcgagt agggctcagg catcacaccc 800  
 acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgaggg 850  
 gggctccccg ccttccacct ggctgtcatc gggtagggcg gggccgtggg 900  
 ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctggcgag 950  
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 gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
 cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100  
 ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150  
 gcggctgcag tccttttctc cctcaaaggc ctccgacct cagctggagg 1200  
 cgggcatctt tcctaaaggg tcccatagg gtctggttcc accccatccc 1250  
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 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
 125 130 135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro  
155

&lt;210&gt; 357

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

B1

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cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

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ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400  
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450  
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caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 358

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu  
1 5 10 15  
Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser  
20 25 30  
Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp  
35 40 45  
Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val  
50 55 60  
Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu  
65 70 75  
His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser  
80 85 90  
Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr  
95 100 105  
Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu  
110 115 120  
Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe  
125 130 135  
Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val  
140 145 150  
Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu  
155 160 165  
Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His  
170 175 180  
Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe  
185 190 195

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

B1

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 359  
 ccagcagtgc ccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

B1  
<400> 363  
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cctcagcggg gacccgggct cagggacgcg gcggcggcgg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggctcgt gctggcggcg gcgcttgggc 250  
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300  
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550  
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600  
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgcctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
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gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
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 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
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 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaaggctcact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<400> 364  
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 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
 20 25 30  
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
 35 40 45  
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
 50 55 60  
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
 65 70 75  
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
 80 85 90  
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
 95 100 105



Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile  
 110 115 120  
 Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys  
 125 130 135  
 Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile  
 140 145 150  
 Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val  
 155 160 165  
 Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr  
 170 175 180  
 Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn  
 185 190 195  
 Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser  
 200 205 210  
 Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly  
 215 220 225  
 Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile  
 230 235 240  
 Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile  
 245 250 255  
 Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn  
 260 265

<210> 365  
 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
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 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggcc 150  
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200  
 aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250  
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300  
 agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350  
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 agtgggttga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450  
 gttatgctga tgttgagaac cgtgtacat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttcccattt aagtggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
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 caggaagaaa acgagccagt gatttacaat agagcaagggt aatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 366  
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro  
 1 5 10 15  
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
 20 25 30  
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
 35 40 45  
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
 50 55 60  
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu  
 65 70 75  
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro  
 80 85 90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala  
 95 100 105  
 Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp  
 110 115 120  
 Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly  
 125 130 135  
 Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn  
 140 145 150  
 Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile  
 155 160 165  
 Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala  
 170 175 180  
 Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu  
 185 190 195  
 Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr  
 200 205 210  
 Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys  
 215 220 225  
 Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys  
 230 235 240  
 Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys  
 245 250 255  
 Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu  
 260 265 270  
 Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn  
 275 280 285  
 Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn  
 290 295 300  
 Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe  
 305 310 315  
 Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu  
 320 325 330  
 Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp  
 335 340 345  
 Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val  
 350 355 360  
 Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
 365 370

<210> 367

<211> 30  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-30  
<223> Synthetic construct.

<400> 367  
tggaagagaa gtctgggtcag aaggtttagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 368  
catttggtt cattctcctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 369  
aaaacctcag aacaactcat tttgcacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 370  
gtctcaccat ggttgctctt gccaaattgt ggaagcagg g 41

<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
ctggggcaac ccggtgctc ctgctcttgc tgatggcggg agcagcgccc 150  
agtcgagccc ggggcagcgg ctgccggggc gggactgggtg cgcgaggggc 200  
tggggcggaa ggtcgagagg gcgaggcctg tggcacgggtg gggctgctgc 250  
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300  
tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350  
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
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caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe  
 50 55 60  
 Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu  
 65 70 75  
 Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu  
 80 85 90  
 Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn  
 95 100 105  
 Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp  
 110 115 120  
 Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys  
 125 130 135  
 Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val  
 140 145 150  
 Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro  
 155 160 165  
 Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu  
 170 175 180  
 Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly  
 185 190 195  
 Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala  
 200 205 210  
 Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys  
 215 220 225  
 Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser  
 230 235 240  
 Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly  
 245 250 255  
 Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu  
 260 265

<210> 373  
 <211> 1706  
 <212> DNA  
 <213> Homo sapiens

<400> 373  
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 cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150  
 tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250  
 ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300  
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350  
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
 ctagtggcct cctcccttgt ggattggctg ggctgcaaga attcttgtgt 450  
 cctcttctcc ctgacttact cactatgctg cttaaccaa ctctctcaag 500  
 actactttgt gctgctagtg gggcgagcac ttgggtgggct gtccacagcc 550  
 ctgctcttct cagccttcga ggcctgggtat atccatgagc acgtggaacg 600  
 gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650  
 tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700  
 gccagctgga tagggctggg gcctgtagcg ccctttgttg ctgccatccc 750  
 tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800  
 atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850  
 ctctgtcgg accgccgct gctgctgctg ggcaccatac aagctctatt 900  
 tgagagtgtc atcttcatct ttgtcttct ctggacacct gtgctggacc 950  
 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000  
 ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050  
 tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100  
 tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150  
 tccttcatag cttttctact tattgagttg gcttgtggat tatactttcc 1200  
 cagcatgagc ttctacgga gaaaggatgat ccctgagaca gagcaggctg 1250  
 gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300  
 ctcttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
 cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400  
 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
 gaggagccct atgcccctga gctgtaacct cactccagga caagatagct 1500  
 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser  
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly  
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe  
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala  
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu  
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu  
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala  
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val  
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu  
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn  
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu  
230 235 240



Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile  
 245 250 255  
 Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp  
 260 265 270  
 Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe  
 275 280 285  
 Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg  
 290 295 300  
 Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu  
 305 310 315  
 Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr  
 320 325 330  
 Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile  
 335 340 345  
 Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser  
 350 355 360  
 Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala  
 365 370 375  
 Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys  
 380 385 390  
 Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr  
 395 400 405  
 Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu  
 410 415 420  
 Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu  
 425 430 435  
 Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu  
 440 445 450

<210> 375  
 <211> 1098  
 <212> DNA  
 <213> Artificial

<400> 375  
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50  
 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100  
 gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacgggt 300  
 tcttcatcca ggaccagatt gctctgggtg agaggggggg ctgctccttc 350  
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500  
 gacggctaca tgatccgccc ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750  
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800  
 cccaggggcc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
 ccccagggtt tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900  
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccagggtt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376  
 <211> 188  
 <212> PRT  
 <213> Homo sapiens

<400> 376  
 Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu  
 1 5 10 15  
 Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu  
 20 25 30  
 Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr  
 35 40 45  
 Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr  
 50 55 60  
 Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly  
 65 70 75  
 Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val  
 80 85 90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln  
                     95                    100                    105  
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp  
                     110                    115                    120  
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg  
                     125                    130                    135  
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr  
                     140                    145                    150  
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile  
                     155                    160                    165  
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu  
                     170                    175                    180  
 Leu Gln Pro Pro Trp Thr Phe Trp  
                     185

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Artificial

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val  
 1 5 10 15  
 Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys  
 20 25 30  
 Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly  
 35 40 45  
 Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr  
 50 55 60  
 Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys  
 65 70 75  
 Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile  
 80 85 90  
 His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe  
 95 100 105  
 Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu  
 110 115

<210> 379  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 379  
 ctgcctccac tgctctgtgc tggg 24

<210> 380  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 380  
 cagagcagtg gatgttcccc tggg 24

<210> 381  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggcccagg agagtataaa 50  
ggcgatgtgg aggggtgcccg gcacaaccag acgcccagtc acaggcgaga 100  
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
ctttcctccg gggatgggc atgtacacca gcaaggaccg ctatttctat 450  
tttgggaagc ttgatggcca gatctcctct gcctaccca gccaaagagg 500  
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650  
ggatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1				5				10					15	
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20				25					30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35				40					45	

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln  
 50 55 60  
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly  
 65 70 75  
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr  
 80 85 90  
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met  
 95 100 105  
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly  
 110 115 120  
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val  
 125 130 135  
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly  
 140 145 150  
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro  
 155 160 165  
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg  
 170 175

<210> 384  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
 gctgagcgtg tgccggtac ggggctctcc tgccttctgg gctccaacgc 50  
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100  
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150  
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca ccccccaaaa aaactgtaaa gatgcaaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
 tggtgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400  
 tgtcagcgag ccctgactca ctacagtga gctgacagg gctgtcatgc 450  
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
 acaaaggatg gggttcaatg taattaggct actgagcgga tcagctgtag 550  
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600  
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tataatctgct gggttgcttag 700  
 gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750  
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800  
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950  
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000  
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
 aacctggaac ttttgacact gggatataac cggatccgaa gtttagccag 1100  
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
 cagaaccttt acttgacgtg gaataaaatc agtgtcatag gacagaccat 1250  
 gtccctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300  
 tcgaagcttt cagtggaccc agtggtttcc agtgtgtccc gaatctgcag 1350  
 cgcctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400  
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450  
 aatgcagcag aaatatttgc tccctgttaa actggctgaa aagttttaaa 1500  
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
 ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650  
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700  
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750  
 tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800  
 ctcgatcatc tgctgggttat ctacgtgtca tggaagcggg accctgag 1850  
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900  
 aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950  
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000  
 gggaccctgc acctataaca aatcgggtc cagggagtgt gaggtatgaa 2050  
 ccattgtgat aaaaagagct cttaaagct gggaaataag tgggtgctta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150  
 tctccctctc actttggtgg caagatcctt ccttgtccgt tttagtgcac 2200  
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250  
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300  
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350  
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385  
 <211> 513  
 <212> PRT  
 <213> Homo sapiens

<400> 385

Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala  
 1 5 10 15  
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala  
 20 25 30  
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
 35 40 45  
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
 50 55 60  
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
 65 70 75  
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
 80 85 90  
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
 95 100 105  
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
 110 115 120  
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
 125 130 135  
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
 140 145 150  
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg  
 155 160 165  
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys  
 170 175 180  
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser  
 185 190 195  
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu



200 205 210  
 His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe  
 215 220 225  
 Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys  
 230 235 240  
 Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu  
 245 250 255  
 Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly  
 260 265 270  
 Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu  
 275 280 285  
 Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser  
 290 295 300  
 Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu  
 305 310 315  
 Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe  
 320 325 330  
 Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu  
 335 340 345  
 Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile  
 350 355 360  
 Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu  
 365 370 375  
 Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu  
 380 385 390  
 Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly  
 395 400 405  
 Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile  
 410 415 420  
 Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu  
 425 430 435  
 Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys  
 440 445 450  
 Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys  
 455 460 465  
 Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr  
 470 475 480  
 Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu  
 485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
 500 505 510

Cys Glu Val

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 386  
 ctgggatctg aacagtttcg gggc 24

<210> 387  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 387  
 ggtccccagg acatggtctg tccc 24

<210> 388  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 388  
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
 <211> 1449  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100  
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tctgctgct ggttttggtg 250  
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300  
 gagaccccgga attgattctc acaggcgcac catggcagtt tttgctgttg 350  
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactggt 400  
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttcctgctcc 450  
 atgttttggc cctttaggct ccccacctcc atatgaagaa attgtaaaaa 500  
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650  
 ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700  
 aggcctttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
 attaattgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
 tctgctttta actctttcct agcatggggg ccataaaaat tattataatt 900  
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
 ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200  
 ctccatagtc catagtgttt ctctggagcc tcagggtttg gcattttattg 1250  
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400  
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 390  
 Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr  
 1 5 10 15

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp  
 20 25 30  
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln  
 35 40 45  
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu  
 50 55 60  
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys  
 65 70 75  
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala  
 80 85 90  
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala  
 95 100 105  
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro  
 110 115 120  
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser  
 125 130 135  
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr  
 140 145

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 391  
 cttttcagtg tcacctcagc gatctc 26

<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 392  
 ccaaaacatg gagcaggaac agg 23

<210> 393  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 393  
ccagttgggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394  
<211> 2340  
<212> DNA  
<213> Homo sapiens

B1  
<400> 394  
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50  
accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100  
gacgcagctg acgcccgtt attagctctc gctgcgtcgc ccgggtcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250  
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300  
cttgctgaag atgaagaata tacaatattg aggatatatt tttctttttt 350  
ttttcaagtc ttgatttggt gcttacctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt ttacaatct caagaaaaaa 450  
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatgtggg 500  
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550  
gtcaagttac gtgagcaaata actagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650  
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750  
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800  
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850  
ttgaaaatca ccttggtgct ctccatccac tgtggattat atcctatggc 900  
agaaaagctt tataattgct ggcttaggac agagcaatac ttacaataa 950  
aagctctaca ctttttcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aattttaaag ttatttggtt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggg 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150  
aatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200  
agtatataac acgttttttg gacaagtga gaatgtttta tcattctgtc 1250  
atttgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300  
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350  
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400  
tttgcactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450  
aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500  
attacctatc gtaaacttg gggcaattta ataacagcat taaaatagtt 1550  
gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600  
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650  
aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700  
catatttggg ttaattttgc ttttattata ttgggtctagg aggaaggac 1750  
tttggagaat ggaactcttg aggactttag ccagggtgtat ataataaagg 1800  
tacttttgtg ctgcattaaa ttgcttgga agtggttaaca ttatattata 1850  
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900  
attcatttta tataatggcc acttaaaata agaacttta aatataaac 1950  
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000  
accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050  
atttccttg tagcaaatc aattgccaca tgggtgcccta tatttcatag 2100  
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150  
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200  
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250  
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300  
acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<210> 395  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 395  
Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser  
1 5 10 15

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu  
 20 25 30  
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
 35 40 45  
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
 50 55 60  
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
 65 70 75  
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
 80 85 90  
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
 95 100 105  
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
 110 115 120  
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
 125 130 135  
 Ser Gly Ser Ile Arg  
 140

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
 cgcggccggg ccgcccgggt gagcgtgccg aggcggctgt ggcgcaggct 50  
 tccagcccc accatgccgt ggcccctgct gctgctgctg gccgtgagt 100  
 gggcccagac aaccggcca tgcttccccg ggtgccaatg cgaggtggag 150  
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
 gggccggggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcatc tcaccactg cttcttcccg ctttcgtac ctggagtcgc 400  
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
 agctcacccc tgagcgacgt gaaccttagc caaaccagc tccgggaggt 500  
 ctcaagtgtc gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
 acctctccca caacctcatt caccgcctcg tgccccaccc cagagggcc 600  
 ggctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

B1

ccatgccgtg cccaacctcc gagacttgcc cctgogctac ctgagcctgg 700  
atgggaaccc tctagctgtc attgggtccgg gtgccttcgc ggggctggga 750  
ggccttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800  
gcccagtggc ttcogtgagc taccgggcct gcaggctcctg gacctgtcgg 850  
gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggcctgagc 900  
tccctgcagg agctggacct ttcgggcacc aacctggtgc ccctgcctga 950  
ggogctgctc ctccacctcc cggcactgca gagcgtcagc gtggggccagg 1000  
atgtgcggtg ccgggcgctg gtgcgggagg gcacctaccc ccggaggcct 1050  
ggctccagcc ccaaggtgcc cctgcactgc gtagacaccc gggaatctgc 1100  
tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150  
aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200  
tgtgccaaca ccagtgggga gcccgagggc ctatgtggca gcgtcaccac 1250  
aggagtgtg ggctaggag aggccttggga cctgggagcc acacctagga 1300  
gcaaagtctc acccctttgt ctacgttgct tccccaaacc atgagcagag 1350  
ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400  
cttatccccc aagtgccttc cctcatgcct gggccggcct gaccgcgaat 1450  
gggcagaggg tgggtgggac cccctgctgc agggcagagt tcaggtccac 1500  
tgggctgagt gtccccttgg gcccatggcc cagtcactca ggggcgagtt 1550  
tcttttctaa catagccctt tctttgccat gaggccatga ggcccgttc 1600  
atccttttct atttccttag aaccttaatg gtagaaggaa ttgcaaagaa 1650  
tcaagtccac ccttctcatg tgacagatgg ggaaactgag gccttgagaa 1700  
ggaaaaaggg taatctaagt tcctgcgggc agtggcatga ctggagcaca 1750  
gcctcctgcc tcccagcccg gacccaatgc actttcttgt ctctctaat 1800  
aagccccacc ctccccgcct gggctcccct tgctgccctt gcctgttccc 1850  
cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900  
gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgccc 1950  
ttcggagcct ctggaagctt agggcacatt ggttccagcc tagccagttt 2000  
ctcaccctgg gttgggggtcc cccagcatcc agactggaaa cctaccatt 2050  
ttcccctgag catcctctag atgctgcccc aaggagttgc tgcagttctg 2100



gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150  
 ctggccctga gcacgacagc ccttcttacc ctcccaggaa tgccgtgaaa 2200  
 ggagacaagg tctgcccagc ccatgtctat gctctacccc cagggcagca 2250  
 tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaag 2300  
 ttgttgccctt tttaacggag tgtcactttc aaccggcctc ccctaccct 2350  
 gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaagggtgca 2400  
 tttgttcaact tttgtaatat tgtcctgggc ctgtgttggg gtgttggggg 2450  
 aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500  
 cccacaggg cagtgagctc tgtcttcccc cacctgccta gcccatcatc 2550  
 tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397  
 <211> 353  
 <212> PRT  
 <213> Homo sapiens

<400> 397  
 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln  
 1 5 10 15  
 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr  
 20 25 30  
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser  
 35 40 45  
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr  
 50 55 60  
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu  
 65 70 75  
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp  
 80 85 90  
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser  
 95 100 105  
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu  
 110 115 120  
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp  
 125 130 135  
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala  
 140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser  
 155 160 165  
 His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly  
 170 175 180  
 Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg  
 185 190 195  
 Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu  
 200 205 210  
 Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe  
 215 220 225  
 Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln  
 230 235 240  
 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly  
 245 250 255  
 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala  
 260 265 270  
 Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp  
 275 280 285  
 Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu  
 290 295 300  
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg  
 305 310 315  
 Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly  
 320 325 330  
 Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser  
 335 340 345  
 Ala Ala Arg Gly Pro Thr Ile Leu  
 350

<210> 398  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 398  
 ccctgccagc cgagagcttc acc 23

<210> 399  
 <211> 23  
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagatc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat tccccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccatth gctaagactc tatctggaca gggatattta 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800  
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850  
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900  
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
 acctgcagag gaggcacgac cccaaaccac catctcttta ctgtactagt 1000  
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050  
 tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100  
 atttttgtaa tatctttctg ctattggata tatttattag ttaatatt 1150  
 tattttattt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200  
 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250  
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300  
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 402  
 Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met  
 1 5 10 15  
 Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu  
 20 25 30  
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys  
 35 40 45  
 Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu  
 50 55 60  
 Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu  
 65 70 75  
 Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser  
 80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr  
                             95                            100                            105  
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile  
                             110                            115                            120  
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg  
                             125                            130                            135  
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu  
                             140                            145                            150  
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys  
                             155                            160                            165  
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe  
                             170                            175                            180  
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser  
                             185                            190                            195  
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu  
                             200                            205                            210  
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys  
                             215                            220                            225  
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln  
                             230                            235                            240  
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln  
                             245                            250                            255  
 Trp Met Glu Glu Thr Glu  
                             260

<210> 403  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 403  
 ctctgtggt ctccagattt caggccta 28

<210> 404  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

131  
<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcgat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaattgaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtg agaatgaccc cttgggtcaat ggtgttctgg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala  
 20 25 30  
 Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr  
 35 40 45  
 Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp  
 50 55 60  
 Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala  
 65 70 75  
 Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly  
 80 85 90  
 Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg  
 95 100 105  
 Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser  
 110 115 120  
 Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met  
 125 130 135  
 Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu  
 140 145 150  
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly  
 155 160 165  
 Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile  
 170 175 180  
 Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro  
 185 190 195  
 Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr  
 200 205 210  
 Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu  
 215 220 225  
 Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu  
 230 235 240  
 Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg  
 245 250 255  
 Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr  
 260 265 270  
 Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly  
 275 280 285  
 Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met  
 290 295 300  
 Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
320

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-31  
<223> Synthetic construct.

<400> 407  
cgcggatccc gttatcgtct tgcgctactg c 31

<210> 408  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-34  
<223> Synthetic construct.

<400> 408  
gcggaattct taaaatggac tgactccact catc 34

<210> 409  
<211> 1487  
<212> DNA  
<213> Homo sapiens

<400> 409  
cggaacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50  
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100  
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150  
tagataattt tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200  
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250  
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300  
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350  
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400  
ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450  
tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500  
gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380



tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650  
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700  
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750  
 ttgaaatagt tttatgaaat ttctttatatt ttcattgcat agactgttaa 800  
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850  
 tattcctgag atttagaact tgatctactc cctgagccag gggttacatca 900  
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950  
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000  
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100  
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150  
 aggttgcagt gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200  
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300  
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350  
 ttttttggtta aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400  
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450  
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys  
 1 5 10 15  
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala  
 20 25 30  
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala  
 35 40 45  
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr  
 50 55 60  
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val  
 65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu  
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu  
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala  
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe  
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe  
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr  
155

<210> 411  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 411  
gtttgaggaa gctgggatac 20

<210> 412  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 412  
ccaaactcga gcacctgttc 20

<210> 413  
<211> 40  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 413  
atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414

g ttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50  
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100  
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350  
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400  
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450  
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500  
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550  
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600  
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650  
ctgggacaga aggcatattga catgtactct ggagatgtta tgcacctagt 700  
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750  
acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800  
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850  
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900  
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950  
gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000  
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050  
cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaaggtgct 1100  
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150  
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200  
accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300  
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415

Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala  
 1 5 10 15  
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
 20 25 30  
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
 35 40 45  
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
 50 55 60  
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
 65 70 75  
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
 80 85 90  
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
 95 100 105  
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
 110 115 120  
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
 125 130 135  
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
 140 145 150  
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
 155 160 165  
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
 170 175 180  
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
 185 190 195  
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
 200 205 210  
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
 215 220

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-21  
<223> Synthetic construct.

<400> 416  
gccatagtca cgacatggat g 21

<210> 417  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 417  
ggatggccag agctgctg 18

<210> 418  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 418  
aaagtacaag tgtggcctca tcaagc 26

<210> 419  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 419  
tctgactcct aagtcaggca ggag 24

<210> 420  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 420  
attctctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
.gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

B1  
<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgtcgc tctctctctc tctctctcac tcctccctcc 200  
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250  
gcaccccttc ctgggacact atgttggttct ccgccctcct gctggagggtg 300  
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtgc ccacgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
cactgggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900  
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000  
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050  
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100  
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgttttatttc 1200  
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250  
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300  
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350  
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
ccttcccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450  
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
gaaatcgctg tgttgttaat gcagaganca aactctgttt agttgcaggg 1550  
gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600  
tttccctaga tatactgagg gatctctcct taggataaag agttgctgtt 1650  
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700  
t 1701

<210> 423  
<211> 337  
<212> PRT  
<213> Homo sapiens

<400> 423  
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
1 5 10 15  
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
20 25 30  
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
35 40 45  
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
50 55 60  
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
65 70 75  
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80 85 90  
 Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala  
 95 100 105  
 Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly  
 110 115 120  
 Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His  
 125 130 135  
 Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala  
 140 145 150  
 Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu  
 155 160 165  
 Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His  
 170 175 180  
 Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro  
 185 190 195  
 Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe  
 200 205 210  
 Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val  
 215 220 225  
 Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln  
 230 235 240  
 Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro  
 245 250 255  
 Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn  
 260 265 270  
 Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr  
 275 280 285  
 Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly  
 290 295 300  
 Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile  
 305 310 315  
 Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser  
 320 325 330  
 Ala Gln Ala Thr Thr Glu Ala  
 335

<210> 424  
 <211> 18  
 <212> DNA  
 <213> Artificial



<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 424  
gtaaagtcgc tggccagc 18

<210> 425  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 425  
cccgatctgc ctgctgta 18

<210> 426  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 426  
ctgcactgta tggccattat tgtg 24

<210> 427  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 427  
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens

<400> 428  
aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt .gggactccct cccacaaaac tggctccgga tcagggaaca 200  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaate 300  
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350  
 gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcacctg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
 agcaaattgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg  
 1 5 10 15  
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys  
 20 25 30  
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200					205					

<210> 430  
 <211> 1257  
 <212> DNA  
 <213> Homo Sapien

<400> 430  
 ggagagaggc gcgcgggtga aaggcgcatc gatgcagcct gcggcggcct 50  
 cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100  
 ccgcctccag ctccgcgtg cccggcagcc gggagccatg cgaccccagg 150  
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200  
 ctgcagctgc ccgcgccgtc gagcgccctc gagatcccca aggggaagca 250  
 aaaggcgag ctccggcaga gggagggtgt ggacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350  
 aatgttatcc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600  
 agcgttggtg ttccacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttat ttt ggaccaagga agccctgaaa tgaattcaac 700  
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750  
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
aatttgtaaa tgtaagaat tttttttata tctgttaa ataaaattatt 1250  
tccaaca 1257

<210> 431  
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Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
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Leu Pro Lys

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26  
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Synthetic oligonucleotide probe  
  
452  
ctctccccct cccttttcct ttgttt 26  
  
453  
18  
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Artificial Sequence  
  
Synthetic oligonucleotide probe  
  
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ctctggtgcc cacagtga 18  
  
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Synthetic oligonucleotide probe  
  
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ccatgcctgc tcagccaaga a 21  
  
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